

10/572696
IAP9 Rec'd PCT/PTO 20 MAR 2006

SEQUENCE LISTING

<110> Garvan Institute of Medical Research
<120> Method of modulating bone growth, remodeling and adiposity
<130> 42-000400US
<160> 20
<170> PatentIn version 3.3
<210> 1
<211> 1180
<212> DNA
<213> human neuropeptide Y1 receptor

<220>
<221> CDS
<222> (7)..(1161)

<400> 1
aagctt atg aat tca aca tta ttt tcc cag gtt gaa aat cat tca gtc 48
Met Asn Ser Thr Leu Phe Ser Gln Val Glu Asn His Ser Val
1 5 10

cac tct aat ttc tca gag aag aat gcc cag ctt ctg gct ttt gaa aat 96
His Ser Asn Phe Ser Glu Lys Asn Ala Gln Leu Leu Ala Phe Glu Asn
15 20 25 30

gat gat tgt cat ctg ccc ttg gcc atg ata ttt acc tta gct ctt gct 144
Asp Asp Cys His Leu Pro Leu Ala Met Ile Phe Thr Leu Ala Leu Ala
35 40 45

tat gga gct gtg atc att ctt ggt gtc tct gga aac ctg gcc ttg atc 192
Tyr Gly Ala Val Ile Leu Gly Val Ser Gly Asn Leu Ala Leu Ile
50 55 60

ata atc atc ttg aaa caa aag gag atg aga aat gtt acc aac atc ctg 240
Ile Ile Ile Leu Lys Gln Lys Glu Met Arg Asn Val Thr Asn Ile Leu
65 70 75

att gtg aac ctt tcc ttc tca gac ttg ctt gtc atc atg tgt ctc 288
Ile Val Asn Leu Ser Phe Ser Asp Leu Leu Val Ala Ile Met Cys Leu
80 85 90

ccc ttt aca ttt gtc tac aca tta atg gac cac tgg gtc ttt ggt gag 336
Pro Phe Thr Phe Val Tyr Thr Leu Met Asp His Trp Val Phe Gly Glu
95 100 105 110

gcg atg tgt aag ttg aat cct ttt gtg caa tgt gtt tca atc act gtg 384
Ala Met Cys Lys Leu Asn Pro Phe Val Gln Cys Val Ser Ile Thr Val
115 120 125

tcc att ttc tct ctg gtt ctc att gct gtg gaa cga cat cag ctg ata 432
Ser Ile Phe Ser Leu Val Leu Ala Val Glu Arg His Gln Leu Ile
130 135 140

atc aac cct cga ggg tgg aga cca aat aat aga cat gct tat gta ggt 480

Ile Asn Pro Arg Gly Trp Arg Pro Asn Asn Arg His Ala Tyr Val Gly			
145	150	155	
att gct gtg att tgg gtc ctt gct gtg gct tct tct ttg cct ttc ctg			528
Ile Ala Val Ile Trp Val Leu Ala Val Ala Ser Ser Leu Pro Phe Leu			
160	165	170	
atc tac caa gta atg act gat gag ccg ttc caa aat gta aca ctt gat			576
Ile Tyr Gln Val Met Thr Asp Glu Pro Phe Gln Asn Val Thr Leu Asp			
175	180	185	190
gcg tac aaa gac aaa tac gtg tgc ttt gat caa ttt cca tcg gac tct			624
Ala Tyr Lys Asp Lys Tyr Val Cys Phe Asp Gln Phe Pro Ser Asp Ser			
195	200	205	
cat agg ttg tct tat acc act ctc ctc ttg gtg ctg cag tat ttt ggt			672
His Arg Leu Ser Tyr Thr Leu Leu Leu Val Leu Gln Tyr Phe Gly			
210	215	220	
cca ctt tgt ttt ata ttt att tgc tac ttc aag ata tat ata cgc cta			720
Pro Leu Cys Phe Ile Phe Ile Cys Tyr Phe Lys Ile Tyr Ile Arg Leu			
225	230	235	
aaa agg aga aac aac atg atg gac aag atg aga gac aat aag tac agg			768
Lys Arg Arg Asn Asn Met Met Asp Lys Met Arg Asp Asn Lys Tyr Arg			
240	245	250	
tcc agt gaa acc aaa aga atc aat atc atg ctg ctc tcc att gtg gta			816
Ser Ser Glu Thr Lys Arg Ile Asn Ile Met Leu Leu Ser Ile Val Val			
255	260	265	270
gca ttt gca gtc tgc tgg ctc cct ctt acc atc ttt aac act gtg ttt			864
Ala Phe Ala Val Cys Trp Leu Pro Leu Thr Ile Phe Asn Thr Val Phe			
275	280	285	
gat tgg aat cat cag atc att gct acc tgc aac cac aat ctg tta ttc			912
Asp Trp Asn His Gln Ile Ile Ala Thr Cys Asn His Asn Leu Leu Phe			
290	295	300	
ctg ctc tgc cac ctc aca gca atg ata tcc act tgt gtc aac ccc ata			960
Leu Leu Cys His Leu Thr Ala Met Ile Ser Thr Cys Val Asn Pro Ile			
305	310	315	
ttt tat ggg ttc ctg aac aaa aac ttc cag aga gac ttg cag ttc ttc			1008
Phe Tyr Gly Phe Leu Asn Lys Asn Phe Gln Arg Asp Leu Gln Phe Phe			
320	325	330	
ttc aac ttt tgt gat ttc cgg tct cgg gat gat gat tat gaa aca ata			1056
Phe Asn Phe Cys Asp Phe Arg Ser Arg Asp Asp Asp Tyr Glu Thr Ile			
335	340	345	350
gcc atg tcc acg atg cac aca gat gtt tcc aaa act tct ttg aag caa			1104
Ala Met Ser Thr Met His Thr Asp Val Ser Lys Thr Ser Leu Lys Gln			
355	360	365	
gca agc cca gtc gca ttt aaa aaa atc aac aac aat gat gat aat gaa			1152
Ala Ser Pro Val Ala Phe Lys Lys Ile Asn Asn Asn Asp Asp Asn Glu			
370	375	380	
aaa atc tga aactacttat agctctaga			1180

Lys Ile

<210> 2
<211> 384
<212> PRT
<213> human neuropeptide Y1 receptor

<400> 2

Met Asn Ser Thr Leu Phe Ser Gln Val Glu Asn His Ser Val His Ser
1 5 10 15

Asn Phe Ser Glu Lys Asn Ala Gln Leu Leu Ala Phe Glu Asn Asp Asp
20 25 30

Cys His Leu Pro Leu Ala Met Ile Phe Thr Leu Ala Leu Ala Tyr Gly
35 40 45

Ala Val Ile Ile Leu Gly Val Ser Gly Asn Leu Ala Leu Ile Ile Ile
50 55 60

Ile Leu Lys Gln Lys Glu Met Arg Asn Val Thr Asn Ile Leu Ile Val
65 70 75 80

Asn Leu Ser Phe Ser Asp Leu Leu Val Ala Ile Met Cys Leu Pro Phe
85 90 95

Thr Phe Val Tyr Thr Leu Met Asp His Trp Val Phe Gly Glu Ala Met
100 105 110

Cys Lys Leu Asn Pro Phe Val Gln Cys Val Ser Ile Thr Val Ser Ile
115 120 125

Phe Ser Leu Val Leu Ile Ala Val Glu Arg His Gln Leu Ile Ile Asn
130 135 140

Pro Arg Gly Trp Arg Pro Asn Asn Arg His Ala Tyr Val Gly Ile Ala
145 150 155 160

Val Ile Trp Val Leu Ala Val Ala Ser Ser Leu Pro Phe Leu Ile Tyr
165 170 175

Gln Val Met Thr Asp Glu Pro Phe Gln Asn Val Thr Leu Asp Ala Tyr
180 185 190

Lys Asp Lys Tyr Val Cys Phe Asp Gln Phe Pro Ser Asp Ser His Arg

195

200

205

Leu Ser Tyr Thr Thr Leu Leu Leu Val Leu Gln Tyr Phe Gly Pro Leu
210 215 220

Cys Phe Ile Phe Ile Cys Tyr Phe Lys Ile Tyr Ile Arg Leu Lys Arg
225 230 235 240

Arg Asn Asn Met Met Asp Lys Met Arg Asp Asn Lys Tyr Arg Ser Ser
245 250 255

Glu Thr Lys Arg Ile Asn Ile Met Leu Leu Ser Ile Val Val Ala Phe
260 265 270

Ala Val Cys Trp Leu Pro Leu Thr Ile Phe Asn Thr Val Phe Asp Trp
275 280 285

Asn His Gln Ile Ile Ala Thr Cys Asn His Asn Leu Leu Phe Leu Leu
290 295 300

Cys His Leu Thr Ala Met Ile Ser Thr Cys Val Asn Pro Ile Phe Tyr
305 310 315 320

Gly Phe Leu Asn Lys Asn Phe Gln Arg Asp Leu Gln Phe Phe Phe Asn
325 330 335

Phe Cys Asp Phe Arg Ser Arg Asp Asp Asp Tyr Glu Thr Ile Ala Met
340 345 350

Ser Thr Met His Thr Asp Val Ser Lys Thr Ser Leu Lys Gln Ala Ser
355 360 365

Pro Val Ala Phe Lys Lys Ile Asn Asn Asn Asp Asp Asn Glu Lys Ile
370 375 380

<210> 3
<211> 3747
<212> DNA
<213> human neuropeptide Y2 receptor

<220>
<221> CDS
<222> (496)..(1638)

<400> 3
gaattcggcc gctgagagac cctggacact gttcctgctc cctcgccacc aaaacttctc 60

ctccagtcgg	ctccatgcgc	ccgcagcctc	tgcacctgtt	ttcttgtgtt	120												
taagggtggg	gtttgcccccc	ctccccacgc	tcccatctct	gatcctccca	ccttcacccg	180											
cccaccccg	gagtgagtgc	ggtgcccagg	cgcgcttggc	ctgagaggtc	ggcagcagac	240											
ccggcagcgc	caaccgcccc	gccgctctga	ctgctccggc	tgcccgcccc	cgcggcgcgg	300											
gctgtcctgg	accctaggag	gggacggaac	cggacttgcc	tttgggcacc	ttccagggcc	360											
ctctccaggt	cggctggcta	atcatcgac	agacggactg	cacacatctt	gtttccgcgt	420											
ctccgcaaaa	acgcgaggtc	caggtcagtt	gtagactctt	gtgctggttg	caggccaaagt	480											
ggacctgtac	tgaaa	atg	ggt	cca	ata	ggt	gca	gag	gct	gat	gag	aac	cag	531			
		Met	Gly	Pro	Ile	Gly	Ala	Glu	Ala	Asp	Glu	Asn	Gln				
		1			5					10							
aca	gtg	gaa	gaa	atg	aag	gtg	gaa	caa	ta	c	ggg	cca	caa	aca	act	cct	579
Thr	Val	Glu	Glu	Met	Lys	Val	Glu	Gln	Tyr	Gly	Pro	Gln	Thr	Thr	Pro		
15					20					25							
aga	ggt	gaa	ctg	gtc	cct	gac	cct	gag	cca	gag	ctt	ata	gat	agt	acc	627	
Arg	Gly	Glu	Leu	Val	Pro	Asp	Pro	Glu	Pro	Glu	Ile	Asp	Ser	Thr			
30					35					40							
aag	ctg	att	gag	gta	caa	gtt	gtt	ctc	ata	ttg	gcc	tac	tgc	tcc	atc	675	
Lys	Leu	Ile	Glu	Val	Gln	Val	Val	Leu	Ile	Leu	Ala	Tyr	Cys	Ser	Ile		
45					50					55					60		
atc	ttg	ctt	ggg	gta	att	ggc	aac	tcc	ttg	gtg	atc	cat	gtg	gtg	atc	723	
Ile	Leu	Leu	Gly	Val	Ile	Gly	Asn	Ser	Leu	Val	Ile	His	Val	Val	Ile		
65					70					75							
aaa	ttc	aag	agc	atg	cgc	aca	gta	acc	aac	ttt	ttc	att	gcc	aat	ctg	771	
Lys	Phe	Lys	Ser	Met	Arg	Thr	Val	Thr	Asn	Phe	Phe	Ile	Ala	Asn	Leu		
80					85					90							
gct	gtg	gca	gat	ctt	ttg	gtg	aac	act	ctg	tgt	cta	ccg	ttc	act	ctt	819	
Ala	Val	Ala	Asp	Leu	Leu	Val	Asn	Thr	Leu	Cys	Leu	Pro	Phe	Thr	Leu		
95					100					105							
acc	tat	acc	tta	atg	ggg	gag	tgg	aaa	atg	ggt	cct	gtc	ctg	tgc	cac	867	
Thr	Tyr	Thr	Leu	Met	Gly	Glu	Trp	Lys	Met	Gly	Pro	Val	Leu	Cys	His		
110					115					120							
ctg	gtg	ccc	tat	gcc	cag	ggc	ctg	gca	gta	caa	gta	tcc	aca	atc	acc	915	
Leu	Val	Pro	Tyr	Ala	Gln	Gly	Leu	Ala	Val	Gln	Val	Ser	Thr	Ile	Thr		
125					130					135					140		
ttg	aca	gta	att	gcc	ctg	gac	cg	cac	agg	tgc	atc	gtc	tac	cac	cta	963	
Leu	Thr	Val	Ile	Ala	Leu	Asp	Arg	His	Arg	Cys	Ile	Val	Tyr	His	Leu		
145					150					155							
gag	agc	aag	atc	tcc	aag	cga	atc	agc	ttc	ctg	att	att	ggc	ttg	gcc	1011	
Glu	Ser	Lys	Ile	Ser	Lys	Arg	Ile	Ser	Phe	Leu	Ile	Ile	Gly	Leu	Ala		
160					165					170							
tgg	ggc	atc	agt	gcc	ctg	gca	agt	ccc	ctg	gcc	atc	ttc	cg	gag	1059		
Trp	Gly	Ile	Ser	Ala	Leu	Leu	Ala	Ser	Pro	Leu	Ala	Ile	Phe	Arg	Glu		

175	180	185	
tat tcg ctg att gag atc att ccg gac ttt gag att gtg gcc tgt act Tyr Ser Leu Ile Glu Ile Ile Pro Asp Phe Glu Ile Val Ala Cys Thr 190	195	200	1107
gaa aag tgg cct ggc gag gag aag agc atc tat ggc act gtc tat agt Glu Lys Trp Pro Gly Glu Glu Lys Ser Ile Tyr Gly Thr Val Tyr Ser 205	210	215	1155
ctt tct tcc ttg atc ttg tat gtt ttg cct ctg ggc att ata tca Leu Ser Ser Leu Leu Ile Leu Tyr Val Leu Pro Leu Gly Ile Ile Ser 225	230	235	1203
ttt tcc tac act cgc att tgg agt aaa ttg aag aac cat gtc agt cct Phe Ser Tyr Thr Arg Ile Trp Ser Lys Leu Lys Asn His Val Ser Pro 240	245	250	1251
gga gct gca aat gac cac tac cat cag cga agg caa aaa acc acc aaa Gly Ala Ala Asn Asp His Tyr His Gln Arg Arg Gln Lys Thr Thr Lys 255	260	265	1299
atg ctg gtg tgt gtg gtg gtg ttt gcg gtc agc tgg ctg cct ctc Met Leu Val Cys Val Val Val Phe Ala Val Ser Trp Leu Pro Leu 270	275	280	1347
cat gcc ttc cag ctt gcc gtt gac att gac agc cag gtc ctg gac ctg His Ala Phe Gln Leu Ala Val Asp Ile Asp Ser Gln Val Leu Asp Leu 285	290	295	1395
aag gag tac aaa ctc atc ttc aca gtg ttc cac att atc gcc atg tgc Lys Glu Tyr Lys Leu Ile Phe Thr Val Phe His Ile Ile Ala Met Cys 305	310	315	1443
tcc act ttt gcc aat ccc ctt ctc tat ggc tgg atg aac agc aac tac Ser Thr Phe Ala Asn Pro Leu Leu Tyr Gly Trp Met Asn Ser Asn Tyr 320	325	330	1491
aga aag gct ttc ctc tcg gcc ttc cgc tgt gag cag cgg ttg gat gcc Arg Lys Ala Phe Leu Ser Ala Phe Arg Cys Glu Gln Arg Leu Asp Ala 335	340	345	1539
att cac tct gag gtg tcc gtg aca ttc aag gct aaa aag aac ctg gag Ile His Ser Glu Val Ser Val Thr Phe Lys Ala Lys Lys Asn Leu Glu 350	355	360	1587
gtc aga aag aac agt ggc ccc aat gac tct ttc aca gag gct acc aat Val Arg Lys Asn Ser Gly Pro Asn Asp Ser Phe Thr Glu Ala Thr Asn 365	370	375	1635
gtc taaggaagct gtgggtgaa aatgtatgga tgaattctga ccagagctat Val			1688
gaatctgggtt gatggcggct cacaagtcaa aactgatttc ccattttaaa gaagaagtgg atctaaatgg aagcatctgc tggtaattc ctggaaaact ggctggcag agcctgtgt aaaatactgg aattcaaaga taaggcaaca aaatggttt cttAACAGTT ggTTGGGTAG			1748 1808 1868

tagttgcata	tatgagtaaa	agcagagaga	agtacttttgc	attat	tttcc	tggagtgaag	1928								
aaaactt	gaa	caagaaatttgc	gtattatcaa	agcattgctg	agagacgg	tg	ggaaaataag	1988							
ttgactt	ca	aatcacgtt	ggac	ctggat	tgaggagg	tg	cagttcgc	tgctccctgc	2048						
ttggctt	at	atg	aaaacaccac	tga	acagaaa	tttctcc	agg	gagccacagg	ctctc	c	ttca	2108			
tcgcattt	tg	at	ttttttgt	tcatt	ctcta	gacaaaatcc	atc	aggaaat	gct	gcaggaa	2168				
acgatt	gcca	actata	cgaa	tgg	cttcgag	gagataa	act	gaaatttgc	atata	attaa	2228				
tat	tttggca	gat	gat	taggg	gaact	cctca	acact	cagt	gcca	attgt	tct	aaaacc	2288		
aatt	gcacgt	tt	ggt	gaaag	ttt	ctcaac	tct	gaatca	aag	ctgaaat	tct	cagaatt	2348		
acaggaaat	g	caa	accatca	ttt	aatttct	aatttca	aa	g	taat	ccgct	ttat	ggagat	2408		
actat	ttt	aga	taa	aca	acttgat	acttttatt	ttt	atac	ttt	ttga	acat	gt	2468		
atgattt	c	tct	ttt	ttt	tttcc	tatt	ggag	ct	tttgc	tttgc	tttgc	tttgc	2528		
ctagaga	ata	ttt	gtt	gtt	gtt	cat	gtt	gtt	cat	ttt	ttt	ttt	tttgc	2588	
acaggt	acat	ag	ct	ct	cat	tatt	aa	ga	act	ccat	ttt	ttt	tttgc	2648	
tcctcc	acgg	acc	catt	cat	act	aa	aa	aa	aa	aa	ttt	ttt	tttgc	2708	
tgtaa	gag	act	aaa	aca	ctgg	att	cat	ttc	at	tttgc	tttgc	tttgc	tttgc	2768	
gttt	cacata	ag	ttt	ttt	tttca	aa	ata	ttt	at	tttgc	tttgc	tttgc	tttgc	2828	
aatat	ata	taa	aa	attt	tttgc	aa	ata	tttgc	aa	tttgc	tttgc	tttgc	tttgc	2888	
ttt	attata	tt	at	gaata	aa	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	2948	
ac	tttctat	tc	tca	aaaa	ata	aca	act	g	at	gtt	tttgc	tttgc	tttgc	tttgc	3008
gct	at	ttt	catt	tttgc	tttgc	cat	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	3068
taa	agg	ttt	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	3128
gag	ttt	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	3188
cat	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	3248
atg	aaa	acaa	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	3308
atc	tgt	ata	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	3368
taa	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	3428
ttaa	agg	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	3488
tgt	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	3548
ttat	cca	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	3608
gca	at	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	3668

aaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa 3728

aaaaaaaaaaa aaaaaaaaaaaa 3747

<210> 4
<211> 381
<212> PRT
<213> human neuropeptide Y2 receptor

<400> 4

Met Gly Pro Ile Gly Ala Glu Ala Asp Glu Asn Gln Thr Val Glu Glu
1 5 10 15

Met Lys Val Glu Gln Tyr Gly Pro Gln Thr Thr Pro Arg Gly Glu Leu
20 25 30

Val Pro Asp Pro Glu Pro Glu Leu Ile Asp Ser Thr Lys Leu Ile Glu
35 40 45

Val Gln Val Val Leu Ile Leu Ala Tyr Cys Ser Ile Ile Leu Leu Gly
50 55 60

Val Ile Gly Asn Ser Leu Val Ile His Val Val Ile Lys Phe Lys Ser
65 70 75 80

Met Arg Thr Val Thr Asn Phe Phe Ile Ala Asn Leu Ala Val Ala Asp
85 90 95

Leu Leu Val Asn Thr Leu Cys Leu Pro Phe Thr Leu Thr Tyr Thr Leu
100 105 110

Met Gly Glu Trp Lys Met Gly Pro Val Leu Cys His Leu Val Pro Tyr
115 120 125

Ala Gln Gly Leu Ala Val Gln Val Ser Thr Ile Thr Leu Thr Val Ile
130 135 140

Ala Leu Asp Arg His Arg Cys Ile Val Tyr His Leu Glu Ser Lys Ile
145 150 155 160

Ser Lys Arg Ile Ser Phe Leu Ile Ile Gly Leu Ala Trp Gly Ile Ser
165 170 175

Ala Leu Leu Ala Ser Pro Leu Ala Ile Phe Arg Glu Tyr Ser Leu Ile
180 185 190

Glu Ile Ile Pro Asp Phe Glu Ile Val Ala Cys Thr Glu Lys Trp Pro
195 200 205

Gly Glu Glu Lys Ser Ile Tyr Gly Thr Val Tyr Ser Leu Ser Ser Leu
210 215 220

Leu Ile Leu Tyr Val Leu Pro Leu Gly Ile Ile Ser Phe Ser Tyr Thr
225 230 235 240

Arg Ile Trp Ser Lys Leu Lys Asn His Val Ser Pro Gly Ala Ala Asn
245 250 255

Asp His Tyr His Gln Arg Arg Gln Lys Thr Thr Lys Met Leu Val Cys
260 265 270

Val Val Val Val Phe Ala Val Ser Trp Leu Pro Leu His Ala Phe Gln
275 280 285

Leu Ala Val Asp Ile Asp Ser Gln Val Leu Asp Leu Lys Glu Tyr Lys
290 295 300

Leu Ile Phe Thr Val Phe His Ile Ile Ala Met Cys Ser Thr Phe Ala
305 310 315 320

Asn Pro Leu Leu Tyr Gly Trp Met Asn Ser Asn Tyr Arg Lys Ala Phe
325 330 335

Leu Ser Ala Phe Arg Cys Glu Gln Arg Leu Asp Ala Ile His Ser Glu
340 345 350

Val Ser Val Thr Phe Lys Ala Lys Lys Asn Leu Glu Val Arg Lys Asn
355 360 365

Ser Gly Pro Asn Asp Ser Phe Thr Glu Ala Thr Asn Val
370 375 380

<210> 5
<211> 2260
<212> DNA
<213> human neuorpeptide Y4 receptor

<220>
<221> CDS
<222> (660)..(1787)

<400> 5
ggatccccga ggcttagct ctatctgaa gggatgggg tgccgtggaa ggacacaagc 60

aatcctgtgc tgagtggcat ttattgctgt ctccattcag ataaaatgtg acaagggca	120
ttctacccat gttccctgaa caattccgtc actaaagtct gcatacagca ctccaactt	180
tttacatca gaacagcctc atcctgaggc ggagggatt agtagaaacaa gttctggcat	240
tagatgacct gagttttaa ctgggcctgt tactaattag ctgtgtgact atgggcaagt	300
tgcttccat ctcagggtct tagattcctc atctatgaaa cggattgata atatctacct	360
ctaggaataa actagcta atagctaa agacgaaagt gctgagcaca gtacccagca tgcaacaagt	420
gcttctaaca aggttagcaat cattggatgc caatgtctca ccatgagcct taggtaatag	480
ccctccagat accagccttg gtttggaaagc agctgagagc ctttctaccc ggcctgctc	540
ctctctggat tctaccctgg gcatgatccc tgagtattgt ttgtctgttt gcctttagg	600
gcgtcatccc tcaagtgtat cacttagttc aagagtccctg gaatctttc acatccact	659
atg aac acc tct cac ctc ctg gcc ttg ctg ctc cca aaa tct cca caa Met Asn Thr Ser His Leu Leu Ala Leu Leu Leu Pro Lys Ser Pro Gln	707
1 5 10 15	
ggt gaa aac aga agc aaa ccc ctg ggc acc cca tac aac ttc tct gaa Gly Glu Asn Arg Ser Lys Pro Leu Gly Thr Pro Tyr Asn Phe Ser Glu	755
20 25 30	
cat tgc cag gat tcc gtg gac gtg atg gtc ttc atc gtc act tcc tac His Cys Gln Asp Ser Val Asp Val Met Val Phe Ile Val Thr Ser Tyr	803
35 40 45	
agc att gag act gtc gtg ggg gtc ctg ggt aac ctc tgc ctg atg tgt Ser Ile Glu Thr Val Val Gly Val Leu Gly Asn Leu Cys Leu Met Cys	851
50 55 60	
gtg act gtg agg cag aag gag aaa gcc aac gtg acc aac ctg ctt atc Val Thr Val Arg Gln Lys Glu Lys Ala Asn Val Thr Asn Leu Leu Ile	899
65 70 75 80	
gcc aac ctg gcc ttc tct gac ttc ctc atg tgc ctc ctc tgc cag ccg Ala Asn Leu Ala Phe Ser Asp Phe Leu Met Cys Leu Leu Cys Gln Pro	947
85 90 95	
ctg acc gcc gtc tac acc atc atg gac tac tgg atc ttt gga gag acc Leu Thr Ala Val Tyr Thr Ile Met Asp Tyr Trp Ile Phe Gly Glu Thr	995
100 105 110	
ctc tgc aag atg tcg gcc ttc atc cag tgc atg tcg gtg acg gtc tcc Leu Cys Lys Met Ser Ala Phe Ile Gln Cys Met Ser Val Thr Val Ser	1043
115 120 125	
atc ctc tcg ctc gtc ctc gtg gcc ctg gag agg cat cag ctc atc atc Ile Leu Ser Leu Val Leu Val Ala Leu Glu Arg His Gln Leu Ile Ile	1091
130 135 140	
aac cca aca ggc tgg aag ccc agc atc tca cag gcc tac ctg ggg att Asn Pro Thr Gly Trp Lys Pro Ser Ile Ser Gln Ala Tyr Leu Gly Ile	1139
145 150 155 160	

gtg ctc atc tgg gtc att gcc tgt gtc ctc tcc ctg ccc ttc ctg gcc Val Leu Ile Trp Val Ile Ala Cys Val Leu Ser Leu Pro Phe Leu Ala 165 170 175	1187
aac agc atc ctg gag aat gtc ttc cac aag aac cac tcc aag gct ctg Asn Ser Ile Leu Glu Asn Val Phe His Lys Asn His Ser Lys Ala Leu 180 185 190	1235
gag ttc ctg gca gat aag gtg gtc tgt acc gag tcc tgg cca ctg gct Glu Phe Leu Ala Asp Lys Val Val Cys Thr Glu Ser Trp Pro Leu Ala 195 200 205	1283
cac cac cgc acc atc tac acc acc ttc ctg ctc ttc cag tac tgc His His Arg Thr Ile Tyr Thr Phe Leu Leu Leu Phe Gln Tyr Cys 210 215 220	1331
ctc cca ctg ggc ttc atc ctg gtc tgt tat gca cgc atc tac cgg cgc Leu Pro Leu Gly Phe Ile Leu Val Cys Tyr Ala Arg Ile Tyr Arg Arg 225 230 235 240	1379
ctg cag agg cag ggg cgc gtg ttt cac aag ggc acc tac agc ttg cga Leu Gln Arg Gln Gly Arg Val Phe His Lys Gly Thr Tyr Ser Leu Arg 245 250 255	1427
gct ggg cac atg aag cag gtc aat gtg gtg ctg gtg gtg atg gtg gtg Ala Gly His Met Lys Gln Val Asn Val Val Leu Val Val Met Val Val 260 265 270	1475
gcc ttt gcc gtg ctc tgg ctg cct ctg cat gtg ttc aac agc ctg gaa Ala Phe Ala Val Leu Trp Leu Pro Leu His Val Phe Asn Ser Leu Glu 275 280 285	1523
gac tgg cac cat gag gcc atc ccc atc tgc cac ggg aac ctc atc ttc Asp Trp His His Glu Ala Ile Pro Ile Cys His Gly Asn Leu Ile Phe 290 295 300	1571
tta gtg tgc cac ttg ctt gcc atg gcc tcc acc tgc gtc aac cca ttc Leu Val Cys His Leu Leu Ala Met Ala Ser Thr Cys Val Asn Pro Phe 305 310 315 320	1619
atc tat ggc ttt ctc aac acc aac ttc aag aag gag atc aag gcc ctg Ile Tyr Gly Phe Leu Asn Thr Asn Phe Lys Lys Glu Ile Lys Ala Leu 325 330 335	1667
gtg ctg act tgc cag cag agc gcc ccc ctg gag gag tcg gag cat ctg Val Leu Thr Cys Gln Gln Ser Ala Pro Leu Glu Glu Ser Glu His Leu 340 345 350	1715
ccc ctg tcc aca gta cat acg gaa gtc tcc aaa ggg tcc ctg agg cta Pro Leu Ser Thr Val His Thr Glu Val Ser Lys Gly Ser Leu Arg Leu 355 360 365	1763
agt ggc agg tcc aat ccc att taa ccaggtctag gtcttctccc tgccatgtcc Ser Gly Arg Ser Asn Pro Ile 370 375	1817
cttgcaggc tcttccactt agctaagtgg gcacactgca agctgggtg gcacccccc atccctggct ttctgggtc cagataggct ggcaagagct gttttgcat ccatttgcatt	1877
	1937

cgtgaagact ggcattttga tacttcagct	gtttgttcct	gggagaattc	tgagcacaga	1997
ttccagaggt cacagtaagc	cttgcagctt	gagctgaaag	atgccagagc	2057
tgctggcagc	aggcagggtt	cattctggtg	acacagcaac	2117
cagggatttc	acctccacca	gtgagaccac	ggggccactg	2177
ttggagtcag	agctctagac	cttggtcaac	tcttcacctc	2237
ggtgcttcag	aagtaaagaa	ttc		2260

<210> 6
 <211> 375
 <212> PRT
 <213> human neuorpeptide Y4 receptor
 <400> 6

Met Asn Thr Ser His Leu Leu Ala	Leu Leu Leu Pro	Lys Ser Pro Gln	
1	5	10	15

Gly Glu Asn Arg Ser Lys Pro	Leu Gly Thr Pro	Tyr Asn Phe Ser Glu	
20	25	30	

His Cys Gln Asp Ser Val Asp	Val Met Val Phe Ile	Val Thr Ser Tyr	
35	40	45	

Ser Ile Glu Thr Val Val Gly	Val Leu Gly Asn Leu	Cys Leu Met Cys	
50	55	60	

Val Thr Val Arg Gln Lys Glu	Lys Ala Asn Val Thr	Asn Leu Leu Ile	
65	70	75	80

Ala Asn Leu Ala Phe Ser Asp	Phe Leu Met Cys Leu	Cys Gln Pro	
85	90	95	

Leu Thr Ala Val Tyr Thr Ile Met Asp	Tyr Trp Ile Phe	Gly Glu Thr	
100	105	110	

Leu Cys Lys Met Ser Ala Phe	Ile Gln Cys Met Ser Val	Thr Val Ser	
115	120	125	

Ile Leu Ser Leu Val Leu Val	Ala Leu Glu Arg His	Gln Leu Ile Ile	
130	135	140	

Asn Pro Thr Gly Trp Lys Pro Ser	Ile Ser Gln Ala	Tyr Leu Gly Ile	
145	150	155	160

Val Leu Ile Trp Val Ile Ala Cys Val Leu Ser Leu Pro Phe Leu Ala
165 170 175

Asn Ser Ile Leu Glu Asn Val Phe His Lys Asn His Ser Lys Ala Leu
180 185 190

Glu Phe Leu Ala Asp Lys Val Val Cys Thr Glu Ser Trp Pro Leu Ala
195 200 205

His His Arg Thr Ile Tyr Thr Thr Phe Leu Leu Leu Phe Gln Tyr Cys
210 215 220

Leu Pro Leu Gly Phe Ile Leu Val Cys Tyr Ala Arg Ile Tyr Arg Arg
225 230 235 240

Leu Gln Arg Gln Gly Arg Val Phe His Lys Gly Thr Tyr Ser Leu Arg
245 250 255

Ala Gly His Met Lys Gln Val Asn Val Val Leu Val Val Met Val Val
260 265 270

Ala Phe Ala Val Leu Trp Leu Pro Leu His Val Phe Asn Ser Leu Glu
275 280 285

Asp Trp His His Glu Ala Ile Pro Ile Cys His Gly Asn Leu Ile Phe
290 295 300

Leu Val Cys His Leu Leu Ala Met Ala Ser Thr Cys Val Asn Pro Phe
305 310 315 320

Ile Tyr Gly Phe Leu Asn Thr Asn Phe Lys Lys Glu Ile Lys Ala Leu
325 330 335

Val Leu Thr Cys Gln Gln Ser Ala Pro Leu Glu Glu Ser Glu His Leu
340 345 350

Pro Leu Ser Thr Val His Thr Glu Val Ser Lys Gly Ser Leu Arg Leu
355 360 365

Ser Gly Arg Ser Asn Pro Ile
370 375

<210> 7
<211> 1423
<212> DNA

<213> human neuropeptide Y5 receptor

<220>

<221> CDS

<222> (71)..(1408)

<400> 7

gaaaggctat cggttaacaac tgacctgcca caaagttaga agaaaggatt gattcaagaa 60

agactataat atg gat tta gag ctc gac gag tat tat aac aag aca ctt 109
Met Asp Leu Glu Leu Asp Glu Tyr Tyr Asn Lys Thr Leu
1 5 10

gcc aca gag aat aat act gct gcc act cgg aat tct gat ttc cca gtc 157
Ala Thr Glu Asn Asn Thr Ala Ala Thr Arg Asn Ser Asp Phe Pro Val
15 20 25

tgg gat gac tat aaa agc agt gta gat gac tta cag tat ttt ctg att 205
Trp Asp Asp Tyr Lys Ser Ser Val Asp Asp Leu Gln Tyr Phe Leu Ile
30 35 40 45

ggg ctc tat aca ttt gta agt ctt ctt ggc ttt atg ggg aat cta ctt 253
Gly Leu Tyr Thr Phe Val Ser Leu Leu Gly Phe Met Gly Asn Leu Leu
50 55 60

att tta atg gct ctc atg aaa aag cgt aat cag aag act acg gta aac 301
Ile Leu Met Ala Leu Met Lys Lys Arg Asn Gln Lys Thr Thr Val Asn
65 70 75

ttc ctc ata ggc aat ctg gcc ttt tct gat atc ttg gtt gtg ctg ttt 349
Phe Leu Ile Gly Asn Leu Ala Phe Ser Asp Ile Leu Val Val Leu Phe
80 85 90

tgc tca cct ttc aca ctg acg tct gtc ttg ctg gat cag tgg atg ttt 397
Cys Ser Pro Phe Thr Leu Thr Ser Val Leu Leu Asp Gln Trp Met Phe
95 100 105

ggc aaa gtc atg tgc cat att atg cct ttt ctt caa tgt gtg tca gtt 445
Gly Lys Val Met Cys His Ile Met Pro Phe Leu Gln Cys Val Ser Val
110 115 120 125

ttg gtt tca act tta att tta ata tca att gcc att gtc agg tat cat 493
Leu Val Ser Thr Leu Ile Leu Ser Ile Ala Ile Val Arg Tyr His
130 135 140

atg ata aaa cat ccc ata tct aat aat tta aca gca aac cat ggc tac 541
Met Ile Lys His Pro Ile Ser Asn Asn Leu Thr Ala Asn His Gly Tyr
145 150 155

ttt ctg ata gct act gtc tgg aca cta ggt ttt gcc atc tgt tct ccc 589
Phe Leu Ile Ala Thr Val Trp Thr Leu Gly Phe Ala Ile Cys Ser Pro
160 165 170

ctt cca gtg ttt cac agt ctt gtg gaa ctt caa gaa aca ttt ggt tca 637
Leu Pro Val Phe His Ser Leu Val Glu Leu Gln Glu Thr Phe Gly Ser
175 180 185

gca ttg ctg agc agc agg tat tta tgt gtt gag tca tgg cca tct gat 685
Ala Leu Leu Ser Ser Arg Tyr Leu Cys Val Glu Ser Trp Pro Ser Asp

190	195	200	205	
tca tac aga att gcc ttt act atc tct tta ttg cta gtt cag tat att				733
Ser Tyr Arg Ile Ala Phe Thr Ile Ser Leu Leu Leu Val Gln Tyr Ile				
210	215	220		
ctg ccc tta gtt tgt ctt act gta agt cat aca agt gtc tgc aga agt				781
Leu Pro Leu Val Cys Leu Thr Val Ser His Thr Ser Val Cys Arg Ser				
225	230	235		
ata agc tgt gga ttg tcc aac aaa gaa aac aga ctt gaa gaa aat gag				829
Ile Ser Cys Gly Leu Ser Asn Lys Glu Asn Arg Leu Glu Glu Asn Glu				
240	245	250		
atg atc aac tta act ctt cat cca tcc aaa aag agt ggg cct cag gtg				877
Met Ile Asn Leu Thr Leu His Pro Ser Lys Lys Ser Gly Pro Gln Val				
255	260	265		
aaa ctc tct ggc agc cat aaa tgg agt tat tca ttc atc aaa aaa cac				925
Lys Leu Ser Gly Ser His Lys Trp Ser Tyr Ser Phe Ile Lys Lys His				
270	275	280	285	
aga aga aga tat agc aag aag aca gca tgt gtg tta cct gct cca gaa				973
Arg Arg Arg Tyr Ser Lys Lys Thr Ala Cys Val Leu Pro Ala Pro Glu				
290	295	300		
aga cct tct caa gag aac cac tcc aga ata ctt cca gaa aac ttt ggc				1021
Arg Pro Ser Gln Glu Asn His Ser Arg Ile Leu Pro Glu Asn Phe Gly				
305	310	315		
tct gta aga agt cag ctc tct tca tcc agt aag ttc ata cca ggg gtc				1069
Ser Val Arg Ser Gln Leu Ser Ser Ser Lys Phe Ile Pro Gly Val				
320	325	330		
ccc act tgc ttt gag ata aaa cct gaa gaa aat tca gat gtt cat gaa				1117
Pro Thr Cys Phe Glu Ile Lys Pro Glu Glu Asn Ser Asp Val His Glu				
335	340	345		
ttg aga gta aaa cgt tct gtt aca aga ata aaa aag aga tct cga agt				1165
Leu Arg Val Lys Arg Ser Val Thr Arg Ile Lys Lys Arg Ser Arg Ser				
350	355	360	365	
gtt ttc tac aga ctg acc ata ctg ata tta gta ttt gct gtt agt tgg				1213
Val Phe Tyr Arg Leu Thr Ile Leu Ile Leu Val Phe Ala Val Ser Trp				
370	375	380		
atg cca cta cac ctt ttc cat gtg gta act gat ttt aat gac aat ctt				1261
Met Pro Leu His Leu Phe His Val Val Thr Asp Phe Asn Asp Asn Leu				
385	390	395		
att tca aat agg cat ttc aag ttg gtg tat tgc att tgt cat ttg ttg				1309
Ile Ser Asn Arg His Phe Lys Leu Val Tyr Cys Ile Cys His Leu Leu				
400	405	410		
ggc atg atg tcc tgt ctt aat cca att cta tat ggg ttt ctt aat				1357
Gly Met Met Ser Cys Cys Leu Asn Pro Ile Leu Tyr Gly Phe Leu Asn				
415	420	425		
aat ggg att aaa gct gat tta gtg tcc ctt ata cac tgt ctt cat atg				1405
Asn Gly Ile Lys Ala Asp Leu Val Ser Leu Ile His Cys Leu His Met				

430

435

440

445

taa taattctcac tgttt

1423

<210> 8

<211> 445

<212> PRT

<213> human neuropeptide Y5 receptor

<400> 8

Met Asp Leu Glu Leu Asp Glu Tyr Tyr Asn Lys Thr Leu Ala Thr Glu
1 5 10 15

Asn Asn Thr Ala Ala Thr Arg Asn Ser Asp Phe Pro Val Trp Asp Asp
20 25 30

Tyr Lys Ser Ser Val Asp Asp Leu Gln Tyr Phe Leu Ile Gly Leu Tyr
35 40 45

Thr Phe Val Ser Leu Leu Gly Phe Met Gly Asn Leu Leu Ile Leu Met
50 55 60

Ala Leu Met Lys Lys Arg Asn Gln Lys Thr Thr Val Asn Phe Leu Ile
65 70 75 80

Gly Asn Leu Ala Phe Ser Asp Ile Leu Val Val Leu Phe Cys Ser Pro
85 90 95

Phe Thr Leu Thr Ser Val Leu Leu Asp Gln Trp Met Phe Gly Lys Val
100 105 110

Met Cys His Ile Met Pro Phe Leu Gln Cys Val Ser Val Leu Val Ser
115 120 125

Thr Leu Ile Leu Ile Ser Ile Ala Ile Val Arg Tyr His Met Ile Lys
130 135 140

His Pro Ile Ser Asn Asn Leu Thr Ala Asn His Gly Tyr Phe Leu Ile
145 150 155 160

Ala Thr Val Trp Thr Leu Gly Phe Ala Ile Cys Ser Pro Leu Pro Val
165 170 175

Phe His Ser Leu Val Glu Leu Gln Glu Thr Phe Gly Ser Ala Leu Leu
180 185 190

Ser Ser Arg Tyr Leu Cys Val Glu Ser Trp Pro Ser Asp Ser Tyr Arg
195 200 205

Ile Ala Phe Thr Ile Ser Leu Leu Val Gln Tyr Ile Leu Pro Leu
210 215 220

Val Cys Leu Thr Val Ser His Thr Ser Val Cys Arg Ser Ile Ser Cys
225 230 235 240

Gly Leu Ser Asn Lys Glu Asn Arg Leu Glu Glu Asn Glu Met Ile Asn
245 250 255

Leu Thr Leu His Pro Ser Lys Lys Ser Gly Pro Gln Val Lys Leu Ser
260 265 270

Gly Ser His Lys Trp Ser Tyr Ser Phe Ile Lys Lys His Arg Arg Arg
275 280 285

Tyr Ser Lys Lys Thr Ala Cys Val Leu Pro Ala Pro Glu Arg Pro Ser
290 295 300

Gln Glu Asn His Ser Arg Ile Leu Pro Glu Asn Phe Gly Ser Val Arg
305 310 315 320

Ser Gln Leu Ser Ser Ser Lys Phe Ile Pro Gly Val Pro Thr Cys
325 330 335

Phe Glu Ile Lys Pro Glu Glu Asn Ser Asp Val His Glu Leu Arg Val
340 345 350

Lys Arg Ser Val Thr Arg Ile Lys Lys Arg Ser Arg Ser Val Phe Tyr
355 360 365

Arg Leu Thr Ile Leu Ile Leu Val Phe Ala Val Ser Trp Met Pro Leu
370 375 380

His Leu Phe His Val Val Thr Asp Phe Asn Asp Asn Leu Ile Ser Asn
385 390 395 400

Arg His Phe Lys Leu Val Tyr Cys Ile Cys His Leu Leu Gly Met Met
405 410 415

Ser Cys Cys Leu Asn Pro Ile Leu Tyr Gly Phe Leu Asn Asn Gly Ile
420 425 430

Lys Ala Asp Leu Val Ser Leu Ile His Cys Leu His Met
435 440 445

<210> 9
<211> 1903
<212> DNA
<213> human neuropeptide Y7 receptor

<220>
<221> CDS
<222> (369) ..(1595)

<400> 9
ctcgagatcc attgtgctct aaaggcctcc ttagtagctg ggactacagg cgcccgccac 60
cacgcctggc taattttttt gtatttttag tagggacggc gtttcactgt gttagccaga 120
tggtctccat ctcccgacct cgtgatccac ccacctcgac ctcccaaagt gctgggattta 180
caggcgtgag accgcgcccc gccaatttcc tttcttagtt gcctctgccc acctcttctc 240
ttctgcttcc atattacagg tttcctcagt tgcgaaattta ggatgttaat tatagttttt 300
gacataacaag aaacatcaaa aagattgaat gtcttaataa gagtgaagca ttagatcag 360
tgactgct atg ttc atc atg aat gag aaa tgg gac aca aac tct tca gaa 410
Met Phe Ile Met Asn Glu Lys Trp Asp Thr Asn Ser Ser Glu
1 5 10
aac tgg cat ccc atc tgg aat gtc aat gac aca aag cat cat ctg tac 458
Asn Trp His Pro Ile Trp Asn Val Asn Asp Thr Lys His His Leu Tyr
15 20 25 30
tca gat att aat att acc tat gtg aac tac tat ctt cac cag cct caa 506
Ser Asp Ile Asn Ile Thr Tyr Val Asn Tyr Tyr Leu His Gln Pro Gln
35 40 45
gtg gca gca atc ttc att att tcc tac ttt ctg atc ttc ttt ttg tgc 554
Val Ala Ala Ile Phe Ile Ile Ser Tyr Phe Leu Ile Phe Phe Leu Cys
50 55 60
atg atg gga aat act gtg gtt tgc ttt att gta atg agg aac aaa cat 602
Met Met Gly Asn Thr Val Val Cys Phe Ile Val Met Arg Asn Lys His
65 70 75
atg cac aca gtc act aat ctc ttc atc tta aac ctg gcc ata agt gat 650
Met His Thr Val Thr Asn Leu Phe Ile Leu Asn Leu Ala Ile Ser Asp
80 85 90
tta cta gtt ggc ata ttc tgc atg cct ata aca ctg ctg gac aat att 698
Leu Leu Val Gly Ile Phe Cys Met Pro Ile Thr Leu Leu Asp Asn Ile
95 100 105 110
ata gca gga tgg cca ttt gga aac acg atg tgc aag atc agt gga ttg 746
Ile Ala Gly Trp Pro Phe Gly Asn Thr Met Cys Lys Ile Ser Gly Leu
115 120 125
gtc cag gga ata tct gtc gca gct tca gtc ttt acg tta gtt gca att 794

Val Gln Gly Ile Ser Val Ala Ala Ser Val Phe Thr Leu Val Ala Ile			
130	135	140	
gct gta gat agg ttc cag tgt gtc tac cct ttt aaa cca aag ctc			842
Ala Val Asp Arg Phe Gln Cys Val Val Tyr Pro Phe Lys Pro Lys Leu			
145	150	155	
act atc aag aca gcg ttt gtc att att atg atc atc tgg gtc cta gcc			890
Thr Ile Lys Thr Ala Phe Val Ile Ile Met Ile Ile Trp Val Leu Ala			
160	165	170	
atc acc att atg tct cca tct gca gta atg tta cat gtg caa gaa gaa			938
Ile Thr Ile Met Ser Pro Ser Ala Val Met Leu His Val Gln Glu Glu			
175	180	185	190
aaa tat tac cga gtg aga ctc aac tcc cag aat aaa acc agt cca gtc			986
Lys Tyr Tyr Arg Val Arg Leu Asn Ser Gln Asn Lys Thr Ser Pro Val			
195	200	205	
tac tgg tgc cgg gaa gac tgg cca aat cag gaa atg agg aag atc tac			1034
Tyr Trp Cys Arg Glu Asp Trp Pro Asn Gln Glu Met Arg Lys Ile Tyr			
210	215	220	
acc act gtg ctg ttt gcc aac atc tac ctg gct ccc ctc tcc ctc att			1082
Thr Thr Val Leu Phe Ala Asn Ile Tyr Leu Ala Pro Leu Ser Leu Ile			
225	230	235	
gtc atc atg tat gga agg att gga att tca ctc ttc agg gct gca gtt			1130
Val Ile Met Tyr Gly Arg Ile Gly Ile Ser Leu Phe Arg Ala Ala Val			
240	245	250	
cct cac aca ggc agg aag aac cag gag cag tgg cac gtg gtg tcc agg			1178
Pro His Thr Gly Arg Lys Asn Gln Glu Gln Trp His Val Val Ser Arg			
255	260	265	270
aag aag cag aag atc att aag atg ctc ctg att gtg gcc ctg ctt ttt			1226
Lys Lys Gln Lys Ile Ile Lys Met Leu Leu Ile Val Ala Leu Leu Phe			
275	280	285	
att ctc tca tgg ctg ccc ctg tgg act cta atg atg ctc tca gac tac			1274
Ile Leu Ser Trp Leu Pro Leu Trp Thr Leu Met Met Leu Ser Asp Tyr			
290	295	300	
gct gac ctt tct cca aat gaa ctg cag atc atc aac atc tac atc tac			1322
Ala Asp Leu Ser Pro Asn Glu Leu Gln Ile Ile Asn Ile Tyr Ile Tyr			
305	310	315	
cct ttt gca cac tgg ctg gca ttc ggc aac agc agt gtc aat ccc atc			1370
Pro Phe Ala His Trp Leu Ala Phe Gly Asn Ser Ser Val Asn Pro Ile			
320	325	330	
att tat ggt ttc ttc aac gag aat ttc cgc cgt ggt ttc caa gaa gct			1418
Ile Tyr Gly Phe Phe Asn Glu Asn Phe Arg Arg Gly Phe Gln Glu Ala			
335	340	345	350
ttc cag ctc cag ctc tgc caa aaa aga gca aag cct atg gaa gct tat			1466
Phe Gln Leu Gln Leu Cys Gln Lys Arg Ala Lys Pro Met Glu Ala Tyr			
355	360	365	
acc cta aaa gct aaa agc cat gtg ctc ata aac aca tct aat cag ctt			1514

Thr	Leu	Lys	Ala	Lys	Ser	His	Val	Leu	Ile	Asn	Thr	Ser	Asn	Gln	Leu	
370								375						380		
gtc	cag	gaa	tct	aca	ttt	caa	aac	cct	cat	ggg	gaa	acc	ttg	ctt	tat	1562
Val	Gln	Glu	Ser	Thr	Phe	Gln	Asn	Pro	His	Gly	Glu	Thr	Leu	Leu	Tyr	
385					390							395				
agg	aaa	agt	gct	gaa	aac	ccc	aac	agg	aat	tag	tgatggaaga	attaaaagaa				1615
Arg	Lys	Ser	Ala	Glu	Asn	Pro	Asn	Arg	Asn							
400				405												
actactaaca	gcagtgagat	ttaaaaagag	ctagtgtat	aatcctaact	ctactacgca											1675
ttatatatattt	aaatccattt	ctttttgtgg	ctttgcactt	caaatttttc	aaagaatgtt											1735
ctaaataaaaa	catttactga	aagccctctc	tggcaaaaaaa	attaaaaata	aacaaaaatg											1795
gtcataagat	cataaacaat	cttatgttgt	ataaaaaatac	gtagagtgac	ttagacatgt											1855
ttgcatgaat	aaatatatattt	ctagagaaca	gttaaaaaaaa	aaaaaaaa												1903
<210>	10															
<211>	408															
<212>	PRT															
<213>	human neuropeptide Y7 receptor															
<400>	10															
Met	Phe	Ile	Met	Asn	Glu	Lys	Trp	Asp	Thr	Asn	Ser	Ser	Glu	Asn	Trp	
1				5					10				15			
His	Pro	Ile	Trp	Asn	Val	Asn	Asp	Thr	Lys	His	His	Leu	Tyr	Ser	Asp	
				20				25				30				
Ile	Asn	Ile	Thr	Tyr	Val	Asn	Tyr	Tyr	Leu	His	Gln	Pro	Gln	Val	Ala	
				35			40				45					
Ala	Ile	Phe	Ile	Ile	Ser	Tyr	Phe	Leu	Ile	Phe	Phe	Leu	Cys	Met	Met	
				50			55				60					
Gly	Asn	Thr	Val	Val	Cys	Phe	Ile	Val	Met	Arg	Asn	Lys	His	Met	His	
				65			70			75			80			
Thr	Val	Thr	Asn	Leu	Phe	Ile	Leu	Asn	Leu	Ala	Ile	Ser	Asp	Leu	Leu	
				85			90				95					
Val	Gly	Ile	Phe	Cys	Met	Pro	Ile	Thr	Leu	Leu	Asp	Asn	Ile	Ile	Ala	
				100			105				110					
Gly	Trp	Pro	Phe	Gly	Asn	Thr	Met	Cys	Lys	Ile	Ser	Gly	Leu	Val	Gln	
				115			120				125					

Gly Ile Ser Val Ala Ala Ser Val Phe Thr Leu Val Ala Ile Ala Val
130 135 140

Asp Arg Phe Gln Cys Val Val Tyr Pro Phe Lys Pro Lys Leu Thr Ile
145 150 155 160

Lys Thr Ala Phe Val Ile Ile Met Ile Ile Trp Val Leu Ala Ile Thr
165 170 175

Ile Met Ser Pro Ser Ala Val Met Leu His Val Gln Glu Glu Lys Tyr
180 185 190

Tyr Arg Val Arg Leu Asn Ser Gln Asn Lys Thr Ser Pro Val Tyr Trp
195 200 205

Cys Arg Glu Asp Trp Pro Asn Gln Glu Met Arg Lys Ile Tyr Thr Thr
210 215 220

Val Leu Phe Ala Asn Ile Tyr Leu Ala Pro Leu Ser Leu Ile Val Ile
225 230 235 240

Met Tyr Gly Arg Ile Gly Ile Ser Leu Phe Arg Ala Ala Val Pro His
245 250 255

Thr Gly Arg Lys Asn Gln Glu Gln Trp His Val Val Ser Arg Lys Lys
260 265 270

Gln Lys Ile Ile Lys Met Leu Leu Ile Val Ala Leu Leu Phe Ile Leu
275 280 285

Ser Trp Leu Pro Leu Trp Thr Leu Met Met Leu Ser Asp Tyr Ala Asp
290 295 300

Leu Ser Pro Asn Glu Leu Gln Ile Ile Asn Ile Tyr Ile Tyr Pro Phe
305 310 315 320

Ala His Trp Leu Ala Phe Gly Asn Ser Ser Val Asn Pro Ile Ile Tyr
325 330 335

Gly Phe Phe Asn Glu Asn Phe Arg Arg Gly Phe Gln Glu Ala Phe Gln
340 345 350

Leu Gln Leu Cys Gln Lys Arg Ala Lys Pro Met Glu Ala Tyr Thr Leu
355 360 365

Lys Ala Lys Ser His Val Leu Ile Asn Thr Ser Asn Gln Leu Val Gln
370 375 380

Glu Ser Thr Phe Gln Asn Pro His Gly Glu Thr Leu Leu Tyr Arg Lys
385 390 395 400

Ser Ala Glu Asn Pro Asn Arg Asn
405

<210> 11
<211> 1980
<212> DNA
<213> mouse neuropeptide Y1 receptor

<220>
<221> CDS
<222> (135)..(1283)

<400> 11
aggaaatgaa gaactgagaa ttatcttggc gaatggattc aaatatatgg aataagagta 60
tgctgaagat ttgatccgtt ttgaagaact ataactgtcc atttatctaa tcggtaacaa 120
caaaacataa aaaa atg aac tca act ctg ttc tcc aag gtt gaa aat cac 170
Met Asn Ser Thr Leu Phe Ser Lys Val Glu Asn His
1 5 10
tca att cac tat aat gcc tca gag aat tct cca ctt ctg gct ttt gaa 218
Ser Ile His Tyr Asn Ala Ser Glu Asn Ser Pro Leu Leu Ala Phe Glu
15 20 25
aat gat gac tgc cac ctg ccc ttg gct gtg ata ttc acc ttg gct ctc 266
Asn Asp Asp Cys His Leu Pro Leu Ala Val Ile Phe Thr Leu Ala Leu
30 35 40
gct tat ggg gcg gtg att att ctt ggc gtc tct gga aac ctg gca ttg 314
Ala Tyr Ala Val Ile Ile Leu Gly Val Ser Gly Asn Leu Ala Leu
45 50 55 60
atc ata atc att ctg aaa cag aag gag atg aga aat gtc acc aac att 362
Ile Ile Ile Leu Lys Gln Lys Glu Met Arg Asn Val Thr Asn Ile
65 70 75
ctg atc gtg aac ctc tcc ttc tca gac ttg ctc gtt gcg gtc atg tgt 410
Leu Ile Val Asn Leu Ser Phe Ser Asp Leu Leu Val Ala Val Met Cys
80 85 90
ctc ccg ttc act ttt gta tat aca ctg atg gac cac tgg gtc ttc ggg 458
Leu Pro Phe Thr Phe Val Tyr Thr Leu Met Asp His Trp Val Phe Gly
95 100 105
gag acc atg tgc aaa ctg aat ccc ttt gta cag tgt gtc tcc atc aca 506
Glu Thr Met Cys Lys Leu Asn Pro Phe Val Gln Cys Val Ser Ile Thr
110 115 120

gta tcc att ttc tcg ctg gtt ctc atc gct gtg gaa cgg cat cag cta		554	
Val Ser Ile Phe Ser Leu Val Leu Ile Ala Val Glu Arg His Gln Leu			
125	130	135	140
atc atc aac cca aga ggg tgg aga cca aac aat aga cat gct tac ata		602	
Ile Ile Asn Pro Arg Gly Trp Arg Pro Asn Asn Arg His Ala Tyr Ile			
145	150	155	
ggc att act gtc att tgg gtc ctt gca gtg gct tct tct ctg ccc ttt		650	
Gly Ile Thr Val Ile Trp Val Leu Ala Val Ala Ser Ser Leu Pro Phe			
160	165	170	
gtg atc tat caa att ctg acc gac gag ccc ttc caa aat gtg tca ctt		698	
Val Ile Tyr Gln Ile Leu Thr Asp Glu Pro Phe Gln Asn Val Ser Leu			
175	180	185	
gcg gcg ttc aag gac aag tat gtg tgc ttt gac aaa ttc cca tct gac		746	
Ala Ala Phe Lys Asp Lys Tyr Val Cys Phe Asp Lys Phe Pro Ser Asp			
190	195	200	
tct cac agg ctg tct tac acg act ctc ctc ctg gtg ctg cag tat ttc		794	
Ser His Arg Leu Ser Tyr Thr Leu Leu Leu Val Leu Gln Tyr Phe			
205	210	215	220
ggc cca ctc tgc ttt ata ttc ata tgc tac ttc aag ata tac att cgc		842	
Gly Pro Leu Cys Phe Ile Phe Ile Cys Tyr Phe Lys Ile Tyr Ile Arg			
225	230	235	
ttg aaa agg aga aac aac atg atg gac aag atc cgg gac agt aag tac		890	
Leu Lys Arg Arg Asn Asn Met Met Asp Lys Ile Arg Asp Ser Lys Tyr			
240	245	250	
agg tcc agt gag acc aag cga atc aac atc atg ctg ctc tcc att gtg		938	
Arg Ser Ser Glu Thr Lys Arg Ile Asn Ile Met Leu Leu Ser Ile Val			
255	260	265	
gtc gcc ttc gcc gtc tgc tgg ctg ccc ctt acc atc ttc aac act gtg		986	
Val Ala Phe Ala Val Cys Trp Leu Pro Leu Thr Ile Phe Asn Thr Val			
270	275	280	
ttc gac tgg aac cac cag atc att gcc acc tgc aac cac aat ctg ctg		1034	
Phe Asp Trp Asn His Gln Ile Ile Ala Thr Cys Asn His Asn Leu Leu			
285	290	295	300
ttt ctg ctc tgt cac ctc acc gcc atg atc tcc acc tgc gtc aac ccc		1082	
Phe Leu Leu Cys His Leu Thr Ala Met Ile Ser Thr Cys Val Asn Pro			
305	310	315	
atc ttt tat gga ttc ctg aac aaa aat ttc cag aga gac ttg cag ttc		1130	
Ile Phe Tyr Gly Phe Leu Asn Lys Asn Phe Gln Arg Asp Leu Gln Phe			
320	325	330	
ttc ttc aac ttt tgt gac ttc cgg tct cga gac gat gac tac gag acc		1178	
Phe Phe Asn Phe Cys Asp Phe Arg Ser Arg Asp Asp Asp Tyr Glu Thr			
335	340	345	
ata gcc atg tct acc atg cat acg gat gtg tcc aag acg tct ctg aag		1226	
Ile Ala Met Ser Thr Met His Thr Asp Val Ser Lys Thr Ser Leu Lys			
350	355	360	

cag gct agc cca gtc gca ttt aaa aaa atc agt atg aat gac aat gaa 1274
Gln Ala Ser Pro Val Ala Phe Lys Lys Ile Ser Met Asn Asp Asn Glu
365 370 375 380

aaa gtc tga agctgctcag agcatatggc cccaggccat atctgtggaa 1323
Lys Val

aaacaagcac agcctgccgc atgctttctt tacctatgct ctgggggaac ggaatgaggc 1383
gcgcggaa agcccaggac atctgtgtta aatttgactg cttttgatgg ttgccctgat 1443
tacttagaaa tctagattac tttgtaatct atctctggca acagtttga ctagatgtcc 1503
tgtgtgtgtg tgtgtgtgtg tgtgtgtgtg tgtgtgtgtg tgtgtgtgt 1563
cgcgccgcgc cgccgcacgtg caaaagagaa agagagagag agaaggagag agacagacag 1623
actgcctgtc tgtctgtctg tctgtcttc tttatgtatg tgtttgaatt atgcataatga 1683
caaagagttt tacattgtgt ttgttggagt gaatttctct gaagtaatgt catgagctca 1743
tttcaaaagc agtcaccacc tgatattctc gagaggctga atttcaaga tcagatgaga 1803
tttccgagac cccggactac ctgcgttccc tgctaggcat catcttagtc tgtcacaagg 1863
gtgacagttt acaaagtcac cttttgaat gtgcctgagt caaaagagtg tctgaagtca 1923
tttggcagca tctttcctt ttcctctcta tttctgttaag gactcaattt cttatac 1980

<210> 12
<211> 382
<212> PRT
<213> mouse neuropeptide Y1 receptor

<400> 12

Met Asn Ser Thr Leu Phe Ser Lys Val Glu Asn His Ser Ile His Tyr
1 5 10 15

Asn Ala Ser Glu Asn Ser Pro Leu Leu Ala Phe Glu Asn Asp Asp Cys
20 25 30

His Leu Pro Leu Ala Val Ile Phe Thr Leu Ala Leu Ala Tyr Gly Ala
35 40 45

Val Ile Ile Leu Gly Val Ser Gly Asn Leu Ala Leu Ile Ile Ile Ile
50 55 60

Leu Lys Gln Lys Glu Met Arg Asn Val Thr Asn Ile Leu Ile Val Asn
65 70 75 80

Leu Ser Phe Ser Asp Leu Leu Val Ala Val Met Cys Leu Pro Phe Thr
85 90 95

Phe Val Tyr Thr Leu Met Asp His Trp Val Phe Gly Glu Thr Met Cys
100 105 110

Lys Leu Asn Pro Phe Val Gln Cys Val Ser Ile Thr Val Ser Ile Phe
115 120 125

Ser Leu Val Leu Ile Ala Val Glu Arg His Gln Leu Ile Ile Asn Pro
130 135 140

Arg Gly Trp Arg Pro Asn Asn Arg His Ala Tyr Ile Gly Ile Thr Val
145 150 155 160

Ile Trp Val Leu Ala Val Ala Ser Ser Leu Pro Phe Val Ile Tyr Gln
165 170 175

Ile Leu Thr Asp Glu Pro Phe Gln Asn Val Ser Leu Ala Ala Phe Lys
180 185 190

Asp Lys Tyr Val Cys Phe Asp Lys Phe Pro Ser Asp Ser His Arg Leu
195 200 205

Ser Tyr Thr Thr Leu Leu Leu Val Leu Gln Tyr Phe Gly Pro Leu Cys
210 215 220

Phe Ile Phe Ile Cys Tyr Phe Lys Ile Tyr Ile Arg Leu Lys Arg Arg
225 230 235 240

Asn Asn Met Met Asp Lys Ile Arg Asp Ser Lys Tyr Arg Ser Ser Glu
245 250 255

Thr Lys Arg Ile Asn Ile Met Leu Leu Ser Ile Val Val Ala Phe Ala
260 265 270

Val Cys Trp Leu Pro Leu Thr Ile Phe Asn Thr Val Phe Asp Trp Asn
275 280 285

His Gln Ile Ile Ala Thr Cys Asn His Asn Leu Leu Phe Leu Leu Cys
290 295 300

His Leu Thr Ala Met Ile Ser Thr Cys Val Asn Pro Ile Phe Tyr Gly
305 310 315 320

Phe Leu Asn Lys Asn Phe Gln Arg Asp Leu Gln Phe Phe Asn Phe
325 330 335

Cys Asp Phe Arg Ser Arg Asp Asp Asp Tyr Glu Thr Ile Ala Met Ser
340 345 350

Thr Met His Thr Asp Val Ser Lys Thr Ser Leu Lys Gln Ala Ser Pro
355 360 365

Val Ala Phe Lys Lys Ile Ser Met Asn Asp Asn Glu Lys Val
370 375 380

<210> 13
<211> 2650
<212> DNA
<213> mouse neuropeptide Y2 receptor

<220>
<221> CDS
<222> (781)..(1938)

<400> 13
acagtcaaca cgcgaaaggt ggagaaaagtt gtattggta ggcttattgg ttagaaagac 60
cattcttagtt ggtgacttcc agaccagtga gaaggcctgt ctcaaaaaac aatgtggatg 120
gcacctgagg aatgataacct gagggttgct tttgactata gacacagatg ttcacactga 180
accacccaca cccccccca cacacacacc agaggggggg ggggctttag tgcacaagaa 240
gtgaaagaaa aaaggcgtgt gtgagaatcc agctgttttgc ctttattta atctccaaa 300
gatcaggtgc tcagcacatg cagatgtttg cccctttgtt atattttagg ctgctgtata 360
cttacacatt tcaaacaatt aagtgggtga cactttccctt taagttatg ttttgacttc 420
atagcaatta taaaattgat aaactttattt gcattcattt tgcattaaaa tggaaatttat 480
ttgatctcac tcattgtgga gctgattctc tctctaacag gaaagtgttag ttttgcata 540
atcatagata ttttgaattt ctaggttcat ccattccctag ttgttaatcg acttatgtaa 600
aggatttgct tcatcaagct tttgcaagat ctacagtgtg atgaatcaga acacagctat 660
ccagagagct cactctaaac taaatcaatc cctttagaat gtttctctgt ttcactaact 720
tttttttaat gtcattttta ttatagattt ttgtgttatt tacaggccaa gtgagagtga 780
atg gtt ctg aag atg ggc ccg gta ggt gca gag gca gat gag aat caa 828
Met Val Leu Lys Met Gly Pro Val Gly Ala Glu Ala Asp Glu Asn Gln
1 5 10 15
act gta gaa gtg aaa gtg gag ccc tat ggg cca ggg cac act act cct 876
Thr Val Glu Val Lys Val Glu Pro Tyr Gly Pro Gly His Thr Thr Pro
20 25 30
aga ggt gag ttg ccc cct gat ccg gag ccg gag ctc ata gac agc acc 924

Arg	Gly	Glu	Leu	Pro	Pro	Asp	Pro	Glu	Pro	Glu	Leu	Ile	Asp	Ser	Thr	
35						40						45				
aaa	ctg	gtc	gag	gtg	cag	gtg	atc	ctc	ata	ttg	gcc	tac	tgc	tcc	atc	972
Lys	Leu	Val	Glu	Val	Gln	Val	Ile	Leu	Ile	Leu	Ala	Tyr	Cys	Ser	Ile	
50						55						60				
atc	ttg	cta	ggg	gta	gtt	ggc	aac	tcc	ctg	gta	atc	cat	gtg	gta	atc	1020
Ile	Leu	Leu	Gly	Val	Val	Gly	Asn	Ser	Leu	Val	Ile	His	Val	Val	Ile	
65						70					75			80		
aaa	tcc	aag	agc	atg	cgc	aca	gta	acc	aac	ttt	ttt	att	gcc	aac	ctg	1068
Lys	Phe	Lys	Ser	Met	Arg	Thr	Val	Thr	Asn	Phe	Phe	Ile	Ala	Asn	Leu	
85										90			95			
gct	gtg	gcf	gat	ctt	ttg	gtg	aac	acc	ctg	tgc	ctg	cca	ttc	act	ctt	1116
Ala	Val	Ala	Asp	Leu	Leu	Val	Asn	Thr	Leu	Cys	Leu	Pro	Phe	Thr	Leu	
100						105						110				
acc	tat	acc	ttg	atg	gga	gag	tgg	aaa	atg	ggt	ccg	gtc	ttg	tgc	cat	1164
Thr	Tyr	Thr	Leu	Met	Gly	Glu	Trp	Lys	Met	Gly	Pro	Val	Leu	Cys	His	
115						120					125					
ttg	gtg	ccc	tat	gcc	cag	ggt	ctg	gcf	gta	caa	gtg	tcc	aca	ata	act	1212
Leu	Val	Pro	Tyr	Ala	Gln	Gly	Leu	Ala	Val	Gln	Val	Ser	Thr	Ile	Thr	
130						135					140					
ttg	aca	gtc	att	gct	ctg	gac	cgc	cat	cgt	tgc	att	gtc	tac	cac	ctg	1260
Leu	Thr	Val	Ile	Ala	Leu	Asp	Arg	Cys	Ile	Val	Tyr	His	Leu			
145						150					155		160			
gag	agc	aag	atc	tcc	aag	cga	atc	agc	ttc	ctg	atc	att	ggc	ctg	gcc	1308
Glu	Ser	Lys	Ile	Ser	Lys	Arg	Ile	Ser	Phe	Leu	Ile	Ile	Gly	Leu	Ala	
165									170			175				
tgg	ggc	atc	agc	gct	ctg	gca	agt	cca	ctg	gcc	atc	ttc	cg	gaa		1356
Trp	Gly	Ile	Ser	Ala	Leu	Leu	Ala	Ser	Pro	Leu	Ala	Ile	Phe	Arg	Glu	
180						185						190				
tac	tcc	ctg	att	gag	atc	att	cct	gac	ttt	gag	att	gtg	gcc	tgt	acc	1404
Tyr	Ser	Leu	Ile	Glu	Ile	Ile	Pro	Asp	Phe	Glu	Ile	Val	Ala	Cys	Thr	
195						200					205					
gag	aag	tgg	cct	ggg	gaa	gag	aag	agt	gtg	tat	ggt	aca	gtc	tac	agc	1452
Glu	Lys	Trp	Pro	Gly	Glu	Lys	Ser	Val	Tyr	Gly	Thr	Val	Tyr	Ser		
210						215					220					
ctt	tcc	acc	ctg	ctc	atc	ctg	tac	gtt	ttg	cct	ctg	ggc	atc	ata	tct	1500
Leu	Ser	Thr	Leu	Leu	Ile	Leu	Tyr	Val	Leu	Pro	Leu	Gly	Ile	Ile	Ser	
225						230					235		240			
ttc	tcc	tac	acc	cgt	atc	tgg	agt	aag	ctg	agg	aac	cac	gtc	agt	cct	1548
Phe	Ser	Tyr	Thr	Arg	Ile	Trp	Ser	Lys	Leu	Arg	Asn	His	Val	Ser	Pro	
245									250			255				
gga	gct	gca	agt	gac	cat	tac	cat	cag	cga	agg	cac	aaa	atg	acc	aaa	1596
Gly	Ala	Ala	Ser	Asp	His	Tyr	His	Gln	Arg	Arg	His	Lys	Met	Thr	Lys	
260									265			270				
atg	ctg	gtg	tgc	gtg	gta	gtg	gtg	ttt	gca	gtc	agc	tgg	cta	ccc	ctc	1644

<210> 14
<211> 385
<212> PRT
<213> mouse neuropeptide Y2 receptor

<400> 14

Met Val Leu Lys Met Gly Pro Val Gly Ala Glu Ala Asp Glu Asn Gln
1 5 10 15

Thr Val Glu Val Lys Val Glu Pro Tyr Gly Pro Gly His Thr Thr Pro
20 25 30

Arg Gly Glu Leu Pro Pro Asp Pro Glu Pro Glu Leu Ile Asp Ser Thr
35 40 45

Lys Leu Val Glu Val Gln Val Ile Leu Ile Leu Ala Tyr Cys Ser Ile
50 55 60

Ile Leu Leu Gly Val Val Gly Asn Ser Leu Val Ile His Val Val Ile
65 70 75 80

Lys Phe Lys Ser Met Arg Thr Val Thr Asn Phe Phe Ile Ala Asn Leu
85 90 95

Ala Val Ala Asp Leu Leu Val Asn Thr Leu Cys Leu Pro Phe Thr Leu
100 105 110

Thr Tyr Thr Leu Met Gly Glu Trp Lys Met Gly Pro Val Leu Cys His
115 120 125

Leu Val Pro Tyr Ala Gln Gly Leu Ala Val Gln Val Ser Thr Ile Thr
130 135 140

Leu Thr Val Ile Ala Leu Asp Arg His Arg Cys Ile Val Tyr His Leu
145 150 155 160

Glu Ser Lys Ile Ser Lys Arg Ile Ser Phe Leu Ile Ile Gly Leu Ala
165 170 175

Trp Gly Ile Ser Ala Leu Leu Ala Ser Pro Leu Ala Ile Phe Arg Glu
180 185 190

Tyr Ser Leu Ile Glu Ile Ile Pro Asp Phe Glu Ile Val Ala Cys Thr
195 200 205

Glu Lys Trp Pro Gly Glu Glu Lys Ser Val Tyr Gly Thr Val Tyr Ser
210 215 220

Leu Ser Thr Leu Leu Ile Leu Tyr Val Leu Pro Leu Gly Ile Ile Ser

225 230 235 240

Phe Ser Tyr Thr Arg Ile Trp Ser Lys Leu Arg Asn His Val Ser Pro
245 250 255

Gly Ala Ala Ser Asp His Tyr His Gln Arg Arg His Lys Met Thr Lys
260 265 270

Met Leu Val Cys Val Val Val Phe Ala Val Ser Trp Leu Pro Leu
275 280 285

His Ala Phe Gln Leu Ala Val Asp Ile Asp Ser His Val Leu Asp Leu
290 295 300

Lys Glu Tyr Lys Leu Ile Phe Thr Val Phe His Ile Ile Ala Met Cys
305 310 315 320

Ser Thr Phe Ala Asn Pro Leu Leu Tyr Gly Trp Met Asn Ser Asn Tyr
325 330 335

Arg Lys Ala Phe Leu Ser Ala Phe Arg Cys Glu Gln Arg Leu Asp Ala
340 345 350

Ile His Ser Glu Val Ser Met Thr Phe Lys Ala Lys Lys Asn Leu Glu
355 360 365

Val Lys Lys Asn Asn Gly Pro Thr Asp Ser Phe Ser Glu Ala Thr Asn
370 375 380

Val
385

<210> 15
<211> 1709
<212> DNA
<213> mouse neuropeptide Y4 receptor

<220>
<221> CDS
<222> (204)..(1331)

<400> 15
atgcctgcct cttaccttaa gccttgtatg atagcctcca atgccatgag atataaggcag 60
ccaagaacct tttcccttgc ccttatcggtt acctgggtcc attgttagatg catggcctt 120
gagttccatt tgtttggttt gcaggctgca tctctgaagt agggccctta ctcctggagt 180

tcccgatct tctcacacct acc atg aat acc tct cat ttc ttg gcc cct ctc Met Asn Thr Ser His Phe Leu Ala Pro Leu 1 5 10	233
ttc cca gga tcc cta cag ggt aag aat ggg acc aat cca ttg gat tcc Phe Pro Gly Ser Leu Gln Gly Lys Asn Gly Thr Asn Pro Leu Asp Ser 15 20 25	281
ccc tat aat ttc tct gat ggc tgc cag gat tcg gca gaa ctg ttg gcc Pro Tyr Asn Phe Ser Asp Gly Cys Gln Asp Ser Ala Glu Leu Leu Ala 30 35 40	329
ttc atc atc acc acc tac agc att gag acc atc tta ggg gtc ctg gga Phe Ile Ile Thr Thr Tyr Ser Ile Glu Thr Ile Leu Gly Val Leu Gly 45 50 55	377
aac ctc tgc ttg ata ttt gtg acc aca aga caa aag gaa aag tcc aat Asn Leu Cys Leu Ile Phe Val Thr Thr Arg Gln Lys Glu Lys Ser Asn 60 65 70	425
gtg acc aac cta ctc att gcc aac ctg gcc ttc tct gac ttc ctc atg Val Thr Asn Leu Leu Ile Ala Asn Leu Ala Phe Ser Asp Phe Leu Met 75 80 85 90	473
tgc ctc atc tgc caa cca ctc aca gtc acc tac acc atc atg gat tac Cys Leu Ile Cys Gln Pro Leu Thr Val Thr Tyr Thr Ile Met Asp Tyr 95 100 105	521
tgg atc ttt ggt gaa gtc ctt tgc aag atg tta act ttc atc cag tgt Trp Ile Phe Gly Glu Val Leu Cys Lys Met Leu Thr Phe Ile Gln Cys 110 115 120	569
atg tca gtg aca gtc tcc atc ctc tca ctg gtc ctt gtg gcc ctg gag Met Ser Val Thr Val Ser Ile Leu Ser Leu Val Leu Val Ala Leu Glu 125 130 135	617
aga cac cag ctc att atc aat cca aca ggc tgg aaa ccc agt att ttc Arg His Gln Leu Ile Ile Asn Pro Thr Gly Trp Lys Pro Ser Ile Phe 140 145 150	665
cag gcc tac ctg ggg att gtg gtc atc tgg ttc atc tct tgt ttc ctt Gln Ala Tyr Leu Gly Ile Val Val Ile Trp Phe Ile Ser Cys Phe Leu 155 160 165 170	713
tcc ttg ccg ttc ctg gcc aac agc acc ctg aat gac ctc ttc cac tac Ser Leu Pro Phe Leu Ala Asn Ser Thr Leu Asn Asp Leu Phe His Tyr 175 180 185	761
aac cac tct aag gtt gag ttt ctg gaa gac aag gtc gtc tgc ttt Asn His Ser Lys Val Val Glu Phe Leu Glu Asp Lys Val Val Cys Phe 190 195 200	809
gtg tcc tgg tct tca gat cac cac cgt ctc atc tat acc acc ttt ctg Val Ser Trp Ser Ser Asp His His Arg Leu Ile Tyr Thr Thr Phe Leu 205 210 215	857
ctg ctc ttt cag tac tgc atc cct cta gcc ttc atc ctg gtc tgc tac Leu Leu Phe Gln Tyr Cys Ile Pro Leu Ala Phe Ile Leu Val Cys Tyr 220 225 230	905

ata cgc atc tac cag cgc ctg cag agg cag aag cat gtg ttc cat gcg Ile Arg Ile Tyr Gln Arg Leu Gln Arg Gln Lys His Val Phe His Ala 235 240 245 250	953
cac gct tgc agc tca cga gcg ggg cag atg aag cgg atc aac agc atg His Ala Cys Ser Ser Arg Ala Gly Gln Met Lys Arg Ile Asn Ser Met 255 260 265	1001
ctc atg aca atg gtg act gcc ttt gca gtt ctc tgg cta ccc ctg cat Leu Met Thr Met Val Thr Ala Phe Ala Val Leu Trp Leu Pro Leu His 270 275 280	1049
gtg ttc aac act ctg gag gac tgg tac cag gaa gcc atc cct gct tgc Val Phe Asn Thr Leu Glu Asp Trp Tyr Gln Glu Ala Ile Pro Ala Cys 285 290 295	1097
cat ggc aac ctc atc ttc ttg atg tgc cac ctg ttg gcc atg gct tcc His Gly Asn Leu Ile Phe Leu Met Cys His Leu Leu Ala Met Ala Ser 300 305 310	1145
acc tgt gtc aac cct ttc atc tat ggc ttt ctc aac atc aac ttc aag Thr Cys Val Asn Pro Phe Ile Tyr Gly Phe Leu Asn Ile Asn Phe Lys 315 320 325 330	1193
aag gat atc aag gct ctg gtg ctg acc tgc cat tgc agg tca cct caa Lys Asp Ile Lys Ala Leu Val Leu Thr Cys His Cys Arg Ser Pro Gln 335 340 345	1241
ggg gag tct gag cat ctg ccc ctg tcc act gtt cac acg gac ctc tcc Gly Glu Ser Glu His Leu Pro Leu Ser Thr Val His Thr Asp Leu Ser 350 355 360	1289
aag gga tcg atg agg atg ggt agc aag tct aac ttc ata tag Lys Gly Ser Met Arg Met Gly Ser Lys Ser Asn Phe Ile 365 370 375	1331
ttgtgtctgg gctttccct accattttt ttgacacatc ctttcaactt gttaagaaga	1391
cacattgcag gctgtatag catcctgtca tttctggctt ttggggccca gataggttgg	1451
caagagactt gaagcttggc attcagatgg ttttagccctt tgcttctgag agatctctga	1511
gtcaggattc tgcagatcac agagggact ttgtggctt agctgcaagg gtatttagatg	1571
cagaagtggc tgactctcac agccactcag tacagatgcc tggccaaaa gccttcatct	1631
atgtcctgac cattcagcta acctgcctt ggtgatgtgc ttatgttctt ccaaggatg	1691
ttgggtgttt cagtaggg	1709

<210> 16
 <211> 375
 <212> PRT
 <213> mouse neuropeptide Y4 receptor

<400> 16

Met Asn Thr Ser His Phe Leu Ala Pro Leu Phe Pro Gly Ser Leu Gln
1 5 10 15

Gly Lys Asn Gly Thr Asn Pro Leu Asp Ser Pro Tyr Asn Phe Ser Asp
20 25 30

Gly Cys Gln Asp Ser Ala Glu Leu Leu Ala Phe Ile Ile Thr Thr Tyr
35 40 45

Ser Ile Glu Thr Ile Leu Gly Val Leu Gly Asn Leu Cys Leu Ile Phe
50 55 60

Val Thr Thr Arg Gln Lys Glu Lys Ser Asn Val Thr Asn Leu Leu Ile
65 70 75 80

Ala Asn Leu Ala Phe Ser Asp Phe Leu Met Cys Leu Ile Cys Gln Pro
85 90 95

Leu Thr Val Thr Tyr Thr Ile Met Asp Tyr Trp Ile Phe Gly Glu Val
100 105 110

Leu Cys Lys Met Leu Thr Phe Ile Gln Cys Met Ser Val Thr Val Ser
115 120 125

Ile Leu Ser Leu Val Leu Val Ala Leu Glu Arg His Gln Leu Ile Ile
130 135 140

Asn Pro Thr Gly Trp Lys Pro Ser Ile Phe Gln Ala Tyr Leu Gly Ile
145 150 155 160

Val Val Ile Trp Phe Ile Ser Cys Phe Leu Ser Leu Pro Phe Leu Ala
165 170 175

Asn Ser Thr Leu Asn Asp Leu Phe His Tyr Asn His Ser Lys Val Val
180 185 190

Glu Phe Leu Glu Asp Lys Val Val Cys Phe Val Ser Trp Ser Ser Asp
195 200 205

His His Arg Leu Ile Tyr Thr Phe Leu Leu Leu Phe Gln Tyr Cys
210 215 220

Ile Pro Leu Ala Phe Ile Leu Val Cys Tyr Ile Arg Ile Tyr Gln Arg
225 230 235 240

Leu Gln Arg Gln Lys His Val Phe His Ala His Ala Cys Ser Ser Arg
245 250 255

Ala Gly Gln Met Lys Arg Ile Asn Ser Met Leu Met Thr Met Val Thr
260 265 270

Ala Phe Ala Val Leu Trp Leu Pro Leu His Val Phe Asn Thr Leu Glu
275 280 285

Asp Trp Tyr Gln Glu Ala Ile Pro Ala Cys His Gly Asn Leu Ile Phe
290 295 300

Leu Met Cys His Leu Leu Ala Met Ala Ser Thr Cys Val Asn Pro Phe
305 310 315 320

Ile Tyr Gly Phe Leu Asn Ile Asn Phe Lys Lys Asp Ile Lys Ala Leu
325 330 335

Val Leu Thr Cys His Cys Arg Ser Pro Gln Gly Glu Ser Glu His Leu
340 345 350

Pro Leu Ser Thr Val His Thr Asp Leu Ser Lys Gly Ser Met Arg Met
355 360 365

Gly Ser Lys Ser Asn Phe Ile
370 375

<210> 17
<211> 1868
<212> DNA
<213> mouse neuropeptide Y5 receptor

<220>
<221> CDS
<222> (100)..(1500)

<400> 17
tctagatgtt agttgtgttc tgagtatgtt attgtcatag cgtgctattg ttcttcaagc 60
tgctaatgga cactgtcttc ttccaaaggcag gactcttagt atg gag gtt aaa ctt 114
Met Glu Val Lys Leu
1 5

gaa gag cat ttt aac aag aca ttt gtc acg gag aac aat act gct gcc 162
Glu Glu His Phe Asn Lys Thr Phe Val Thr Glu Asn Asn Thr Ala Ala
10 15 20

agt cag aac acg gcc tcc cct gcc tgg gag gac tac aga ggc aca gag 210
Ser Gln Asn Thr Ala Ser Pro Ala Trp Glu Asp Tyr Arg Gly Thr Glu
25 30 35

aac aat act tct gct gct cgg aac act gcc ttt cca gtc tgg gag gac 258

Asn Asn Thr Ser Ala Ala Arg Asn Thr Ala Phe Pro Val Trp Glu Asp			
40	45	50	
tat aga ggc agc gta gac gac tta caa tac ttc ctg att ggg ctc tat			306
Tyr Arg Gly Ser Val Asp Asp Leu Gln Tyr Phe Leu Ile Gly Leu Tyr			
55	60	65	
aca ttt gta agt ctt ctt ggt ttt atg gga aat cta ctt atc tta atg			354
Thr Phe Val Ser Leu Leu Gly Phe Met Gly Asn Leu Leu Ile Leu Met			
70	75	80	85
gct gtt atg aaa aag cgc aat cag aag act aca gtg aac ttt ctc ata			402
Ala Val Met Lys Lys Arg Asn Gln Lys Thr Thr Val Asn Phe Leu Ile			
90	95	100	
ggc aac ctg gcc ttc tcc gac att ttg gtt gtc ctg ttt tgc tcc cct			450
Gly Asn Leu Ala Phe Ser Asp Ile Leu Val Val Leu Phe Cys Ser Pro			
105	110	115	
ttc acc ctg acc tct gtc ttg ttg gat cag tgg atg ttc ggc aaa gcc			498
Phe Thr Leu Thr Ser Val Leu Leu Asp Gln Trp Met Phe Gly Lys Ala			
120	125	130	
atg tgc cat atc atg cca ttc ctt cag tgt gta tca gtt ctg gtt tca			546
Met Cys His Ile Met Pro Phe Leu Gln Cys Val Ser Val Leu Val Ser			
135	140	145	
act ctg att tta ata tcg att gcc att gtc agg tat cat atg ata aag			594
Thr Leu Ile Leu Ile Ser Ile Ala Ile Val Arg Tyr His Met Ile Lys			
150	155	160	165
cac cct ata tct aac aat tta aca gca aac cat ggc tac ttc ctg ata			642
His Pro Ile Ser Asn Asn Leu Thr Ala Asn His Gly Tyr Phe Leu Ile			
170	175	180	
gct act gtc tgg aca ctg ggc ttt gcc atc tgt tct ccc ctc cca gtg			690
Ala Thr Val Trp Thr Leu Gly Phe Ala Ile Cys Ser Pro Leu Pro Val			
185	190	195	
ttt cac agc ctt gtg gaa ctt aag gaa acc ttt ggc tca gca ttg cta			738
Phe His Ser Leu Val Glu Leu Lys Glu Thr Phe Gly Ser Ala Leu Leu			
200	205	210	
agc agc aag tat ttg tgt gtt gag tca tgg ccc tct gat tca tac aga			786
Ser Ser Lys Tyr Leu Cys Val Glu Ser Trp Pro Ser Asp Ser Tyr Arg			
215	220	225	
att gct ttc aca atc tct tta ttg tta gtt cag tat atc ctg cct cta			834
Ile Ala Phe Thr Ile Ser Leu Leu Val Gln Tyr Ile Leu Pro Leu			
230	235	240	245
gta tgt tta aca gta agt cat act agt gtc tgc agg agt ata agc tgt			882
Val Cys Leu Thr Val Ser His Thr Ser Val Cys Arg Ser Ile Ser Cys			
250	255	260	
gga ttg tcc cac aaa gaa aac aga ctc gaa gaa aat gag atg atc aac			930
Gly Leu Ser His Lys Glu Asn Arg Leu Glu Glu Asn Glu Met Ile Asn			
265	270	275	
tta act cta cat cca tcc aaa aag agt cgg gac cag gca aaa ccc ccc			978

Leu Thr Leu His Pro Ser Lys Lys Ser Arg Asp Gln Ala Lys Pro Pro			
280	285	290	
agc act caa aag tgg agc tac tca ttc atc aga aag cac cga aga agg			1026
Ser Thr Gln Lys Trp Ser Tyr Ser Phe Ile Arg Lys His Arg Arg Arg			
295	300	305	
tac agc aag aag acg gca tgc gtg tta ccc gcc cca gca gga cct tcc			1074
Tyr Ser Lys Lys Thr Ala Cys Val Leu Pro Ala Pro Ala Gly Pro Ser			
310	315	320	325
cag gag aag cac cta acc gtt cca gaa aac cca ggc tcg gtc cgt agc			1122
Gln Glu Lys His Leu Thr Val Pro Glu Asn Pro Gly Ser Val Arg Ser			
330	335	340	
cag ctg tca cca tcc agt aag gtt att cca ggg gtc ccg atc tgc ttt			1170
Gln Leu Ser Pro Ser Ser Lys Val Ile Pro Gly Val Pro Ile Cys Phe			
345	350	355	
gag gtg aaa cct gaa gaa agc tca gat gct cag gag atg aga gtc aag			1218
Glu Val Lys Pro Glu Glu Ser Ser Asp Ala Gln Glu Met Arg Val Lys			
360	365	370	
cgt tcc ctc acg aga ata aag aag aga tct cgc agt gtt ttc tac aga			1266
Arg Ser Leu Thr Arg Ile Lys Lys Arg Ser Arg Ser Val Phe Tyr Arg			
375	380	385	
ctg act ata ttg ata tta gtg ttc gct gtt agc tgg atg cca ctc cac			1314
Leu Thr Ile Leu Ile Leu Val Phe Ala Val Ser Trp Met Pro Leu His			
390	395	400	405
gtc ttc cac gtg gtg acc gat ttc aat gat aac ctg att tcc aat agg			1362
Val Phe His Val Val Thr Asp Phe Asn Asp Asn Leu Ile Ser Asn Arg			
410	415	420	
cat ttc aag ctg gtg tac tgc atc tgt cac ttg tta ggc atg atg tcc			1410
His Phe Lys Leu Val Tyr Cys Ile Cys His Leu Leu Gly Met Met Ser			
425	430	435	
tgt tgt ctt aat ccg atc tta tat gga ttc ctt aat aat ggt atc aaa			1458
Cys Cys Leu Asn Pro Ile Leu Tyr Gly Phe Leu Asn Asn Gly Ile Lys			
440	445	450	
gca gac ttg aga gcc ctt atc cac tgc cta cac atg tca tga			1500
Ala Asp Leu Arg Ala Leu Ile His Cys Leu His Met Ser			
455	460	465	
ttctctctgt gcaccgagga gagaagaaat gtggagactg cccacaatac atctgtgcta			1560
attgatgcat aatttacata aacgtgttct ggatctgaat gccagtttgt aatctatgtat			1620
agatcattta tggtaataatg tggtaattc cgtcaattgt gcagagtcaa tgtcgatcta			1680
aggaaatttc tgtcttgaaa tagttacatt accgtccatt tcatgtcatt ggtaataagt			1740
tgagtgtctt cggtttcgag taaaagttat agctatccaa attgttattt tgtacaaaaaa			1800
tgtaagaagt gaaaaagttg ttccaaagaa tatttaacct cagatttaag gaatttcttt			1860
tatctaga			1868

<210> 18
<211> 466
<212> PRT
<213> mouse neuropeptide Y5 receptor

<400> 18

Met Glu Val Lys Leu Glu Glu His Phe Asn Lys Thr Phe Val Thr Glu
1 5 10 15

Asn Asn Thr Ala Ala Ser Gln Asn Thr Ala Ser Pro Ala Trp Glu Asp
20 25 30

Tyr Arg Gly Thr Glu Asn Asn Thr Ser Ala Ala Arg Asn Thr Ala Phe
35 40 45

Pro Val Trp Glu Asp Tyr Arg Gly Ser Val Asp Asp Leu Gln Tyr Phe
50 55 60

Leu Ile Gly Leu Tyr Thr Phe Val Ser Leu Leu Gly Phe Met Gly Asn
65 70 75 80

Leu Leu Ile Leu Met Ala Val Met Lys Lys Arg Asn Gln Lys Thr Thr
85 90 95

Val Asn Phe Leu Ile Gly Asn Leu Ala Phe Ser Asp Ile Leu Val Val
100 105 110

Leu Phe Cys Ser Pro Phe Thr Leu Thr Ser Val Leu Leu Asp Gln Trp
115 120 125

Met Phe Gly Lys Ala Met Cys His Ile Met Pro Phe Leu Gln Cys Val
130 135 140

Ser Val Leu Val Ser Thr Leu Ile Leu Ile Ser Ile Ala Ile Val Arg
145 150 155 160

Tyr His Met Ile Lys His Pro Ile Ser Asn Asn Leu Thr Ala Asn His
165 170 175

Gly Tyr Phe Leu Ile Ala Thr Val Trp Thr Leu Gly Phe Ala Ile Cys
180 185 190

Ser Pro Leu Pro Val Phe His Ser Leu Val Glu Leu Lys Glu Thr Phe
195 200 205

Gly Ser Ala Leu Leu Ser Ser Lys Tyr Leu Cys Val Glu Ser Trp Pro
210 215 220

Ser Asp Ser Tyr Arg Ile Ala Phe Thr Ile Ser Leu Leu Leu Val Gln
225 230 235 240

Tyr Ile Leu Pro Leu Val Cys Leu Thr Val Ser His Thr Ser Val Cys
245 250 255

Arg Ser Ile Ser Cys Gly Leu Ser His Lys Glu Asn Arg Leu Glu Glu
260 265 270

Asn Glu Met Ile Asn Leu Thr Leu His Pro Ser Lys Lys Ser Arg Asp
275 280 285

Gln Ala Lys Pro Pro Ser Thr Gln Lys Trp Ser Tyr Ser Phe Ile Arg
290 295 300

Lys His Arg Arg Arg Tyr Ser Lys Lys Thr Ala Cys Val Leu Pro Ala
305 310 315 320

Pro Ala Gly Pro Ser Gln Glu Lys His Leu Thr Val Pro Glu Asn Pro
325 330 335

Gly Ser Val Arg Ser Gln Leu Ser Pro Ser Ser Lys Val Ile Pro Gly
340 345 350

Val Pro Ile Cys Phe Glu Val Lys Pro Glu Glu Ser Ser Asp Ala Gln
355 360 365

Glu Met Arg Val Lys Arg Ser Leu Thr Arg Ile Lys Lys Arg Ser Arg
370 375 380

Ser Val Phe Tyr Arg Leu Thr Ile Leu Ile Leu Val Phe Ala Val Ser
385 390 395 400

Trp Met Pro Leu His Val Phe His Val Val Thr Asp Phe Asn Asp Asn
405 410 415

Leu Ile Ser Asn Arg His Phe Lys Leu Val Tyr Cys Ile Cys His Leu
420 425 430

Leu Gly Met Met Ser Cys Cys Leu Asn Pro Ile Leu Tyr Gly Phe Leu
435 440 445

Asn Asn Gly Ile Lys Ala Asp Leu Arg Ala Leu Ile His Cys Leu His
450 455 460

Met Ser
465

<210> 19
<211> 2281
<212> DNA
<213> mouse neuropeptide y6 receptor

<220>
<221> CDS
<222> (823)..(1938)

<400> 19
ctgcagtcta ttggatgaag agtgtacata ttcataataat tcttaaagta ggcagaaatt 60
aaagggatg gaaatatata cttgtactgc cttagatagt caccaggatg ttgttacagt 120
cttcgtttac tgcttctgaa gcctatactg atagaattaa taaaatactg agagagagag 180
agagggacag agagagagag ggggagagag agagagagag agagagagag agagagagag 240
agagagagag agaagagaag aaaacaaggt saagccatct gcttaactta tgtccacatt 300
ctctcaagag cattgtccta tttgtagaat tatctatatt gttaagaatc atctccattg 360
ttaagatttt gtgggctgga gatccagctc tggataaaa gtgcttcct aacatgcatt 420
aagtccctagg ttctattccc aaggctacat aaaaccttgc tttgtatgt atgcctgtaa 480
tcccagtacg cagcaaggag agacaaggag gatcagaagc ttaaggacat cattttgtac 540
atagttagtt tgagggaaagc tgaggatcata tggactctc tctctctcaa aaacaaaaca 600
aaacaaaaca aaaccttcta ctaatattct ggattctgtt tgatttttag gatctcaaga 660
gcatgctgac gtcatttatg tgttccatc agatacagac agagatcata aacatccaac 720
tcattgatta tatgttgaga gttgtccctc aagaaccaat ggccaaacat ccactgagga 780
tacacggaag ctttagaaaat ctctaattaa aatcctgaca ta atg gaa gtg ctc 834
Met Glu Val Leu
1

aca aac cag cca aca cct aat aaa acc agt ggc aag agc aac aac tcg 882
Thr Asn Gln Pro Thr Pro Asn Lys Thr Ser Gly Lys Ser Asn Asn Ser
5 10 15 20

gca ttt ttc tac ttt gaa tcc tgc caa ccc cct ttt cta gcc ata ctc 930
Ala Phe Phe Tyr Phe Glu Ser Cys Gln Pro Pro Phe Leu Ala Ile Leu
25 30 35

ttg cta ctc ata gca tat act gtg atc cta atc atg ggc att ttt gga 978
Leu Leu Leu Ile Ala Tyr Thr Val Ile Leu Ile Met Gly Ile Phe Gly

40	45	50	
aac ctc tct ctt atc atc atc atc ttt aag aaa cag	aga gaa gct caa		1026
Asn Leu Ser Leu Ile Ile Ile Phe Lys Lys Gln Arg	Glu Ala Gln		
55	60	65	
aat gtt acc aac ata ctg att gcc aac ctg tcc ctc	tct gac atc ttg		1074
Asn Val Thr Asn Ile Leu Ile Ala Asn Leu Ser Leu	Ser Asp Ile Leu		
70	75	80	
gtg tgt gtc atg tgc atc cct ttt acg gtc atc tac	act ctg atg gac		1122
Val Cys Val Met Cys Ile Pro Phe Thr Val Ile Tyr	Thr Leu Met Asp		
85	90	95	100
cac tgg gta ttt ggg aac act atg tgt aaa ctc act	tcc tac gtg caa		1170
His Trp Val Phe Gly Asn Thr Met Cys Lys Leu Thr	Ser Tyr Val Gln		
105	110	115	
agt gtc tca gtt tct gtg tcc ata ttc tcc ctt gtg	ttg att gct att		1218
Ser Val Ser Val Ser Ile Phe Ser Leu Val Leu Ile	Ala Ile		
120	125	130	
gaa cga tat cag ctg att gtg aac ccc cgt ggc tgg	aaa ccc aga gta		1266
Glu Arg Tyr Gln Leu Ile Val Asn Pro Arg Gly Trp	Lys Pro Arg Val		
135	140	145	
gct cat gcc tat tgg ggg atc atc ttg att tgg ctc	att tct ctg aca		1314
Ala His Ala Tyr Trp Gly Ile Ile Leu Ile Trp Leu	Ile Ser Leu Thr		
150	155	160	
ttg tct att ccc tta ttc ctg tcc tac cac ctc acc	aat gag ccc ttt		1362
Leu Ser Ile Pro Leu Phe Leu Ser Tyr His Leu Thr	Asn Glu Pro Phe		
165	170	175	180
cat aat ctc tct ctc cct act gac atc tac acc cac	cag gta gct tgt		1410
His Asn Leu Ser Leu Pro Thr Asp Ile Tyr Thr His	Gln Val Ala Cys		
185	190	195	
gtg gag att tgg cct tct aaa ctg aac caa ctc ctc	ttt tct aca tca		1458
Val Glu Ile Trp Pro Ser Lys Leu Asn Gln Leu Leu	Phe Ser Thr Ser		
200	205	210	
tta ttt atg ctc cag tat ttt gtc cct ctg ggt ttc	att ctt atc tgc		1506
Leu Phe Met Leu Gln Tyr Phe Val Pro Leu Gly Phe	Ile Leu Ile Cys		
215	220	225	
tac ctg aag atc gtt ctc tgc ctc cga aaa aga act	agg cag gtg gac		1554
Tyr Leu Lys Ile Val Leu Cys Leu Arg Lys Arg Thr	Arg Gln Val Asp		
230	235	240	
agg aga aag gaa aat aag agc cgt ctc aat gag aac	aag agg gta aat		1602
Arg Arg Lys Glu Asn Lys Ser Arg Leu Asn Glu Asn	Lys Arg Val Asn		
245	250	255	260
gtg atg ttg att tcc atc gta gtg act ttt gga gcc	tgc tgg ttg ccc		1650
Val Met Leu Ile Ser Ile Val Val Thr Phe Gly Ala	Cys Trp Leu Pro		
265	270	275	
ttg aac att ttc aat gtc atc ttc gac tgg tat cat	gag atg ctg atg		1698
Leu Asn Ile Phe Asn Val Ile Phe Asp Trp Tyr His	Glu Met Leu Met		

280

285

290

1746

agc tgc cac cac gac ctg gta ttt gta gtt tgc cac ttg att gct atg
 Ser Cys His His Asp Leu Val Phe Val Val Cys His Leu Ile Ala Met
 295 300 305

1794

gtt tct act tgc ata aat cct ctc ttt tat gga ttt ctc aac aaa aac
 Val Ser Thr Cys Ile Asn Pro Leu Phe Tyr Gly Phe Leu Asn Lys Asn
 310 315 320

1842

ttc cag aag gat cta atg atg ctt att cac cac tgt tgg tgt ggt gaa
 Phe Gln Lys Asp Leu Met Met Leu Ile His His Cys Trp Cys Gly Glu
 325 330 335 340

1890

cct cag gaa agt tat gaa aat att gcc atg tct act atg cac aca gat
 Pro Gln Glu Ser Tyr Glu Asn Ile Ala Met Ser Thr Met His Thr Asp
 345 350 355

1938

gaa tcc aag gga tca tta aaa ctg gct cac ata cca aca ggc ata tag
 Glu Ser Lys Gly Ser Leu Lys Leu Ala His Ile Pro Thr Gly Ile
 360 365 370

1998

aaactggtaa gcaaaatcaa agcccttctg ttatgaaaga aagagaagaa atagtatgga

2058

atagggcaag gtgcagagga agccagactt aaacacataa tatctttggg cccagtttg

2118

ctttaagtta agcatgtcta ctccattcag ccatagaaca cacagagatt tatccctacc

2178

ctttctttt ttcctttgga agaataataa cttaaacaac ctagacatca ttactgagga

2238

agagaacaaa aatgagagag catacaagga cagcagagat gtctgggta caaaattcac

2281

gttattcgct ggaatagcta gaaagttatt agttgtgctg cag

<210> 20

<211> 371

<212> PRT

<213> mouse neuropeptide y6 receptor

<400> 20

Met Glu Val Leu Thr Asn Gln Pro Thr Pro Asn Lys Thr Ser Gly Lys
 1 5 10 15

Ser Asn Asn Ser Ala Phe Phe Tyr Phe Glu Ser Cys Gln Pro Pro Phe
 20 25 30

Leu Ala Ile Leu Leu Leu Ile Ala Tyr Thr Val Ile Leu Ile Met
 35 40 45

Gly Ile Phe Gly Asn Leu Ser Leu Ile Ile Ile Phe Lys Lys Gln
 50 55 60

Arg Glu Ala Gln Asn Val Thr Asn Ile Leu Ile Ala Asn Leu Ser Leu
 65 70 75 80

Ser Asp Ile Leu Val Cys Val Met Cys Ile Pro Phe Thr Val Ile Tyr
85 90 95

Thr Leu Met Asp His Trp Val Phe Gly Asn Thr Met Cys Lys Leu Thr
100 105 110

Ser Tyr Val Gln Ser Val Ser Val Ser Ile Phe Ser Leu Val
115 120 125

Leu Ile Ala Ile Glu Arg Tyr Gln Leu Ile Val Asn Pro Arg Gly Trp
130 135 140

Lys Pro Arg Val Ala His Ala Tyr Trp Gly Ile Ile Leu Ile Trp Leu
145 150 155 160

Ile Ser Leu Thr Leu Ser Ile Pro Leu Phe Leu Ser Tyr His Leu Thr
165 170 175

Asn Glu Pro Phe His Asn Leu Ser Leu Pro Thr Asp Ile Tyr Thr His
180 185 190

Gln Val Ala Cys Val Glu Ile Trp Pro Ser Lys Leu Asn Gln Leu Leu
195 200 205

Phe Ser Thr Ser Leu Phe Met Leu Gln Tyr Phe Val Pro Leu Gly Phe
210 215 220

Ile Leu Ile Cys Tyr Leu Lys Ile Val Leu Cys Leu Arg Lys Arg Thr
225 230 235 240

Arg Gln Val Asp Arg Arg Lys Glu Asn Lys Ser Arg Leu Asn Glu Asn
245 250 255

Lys Arg Val Asn Val Met Leu Ile Ser Ile Val Val Thr Phe Gly Ala
260 265 270

Cys Trp Leu Pro Leu Asn Ile Phe Asn Val Ile Phe Asp Trp Tyr His
275 280 285

Glu Met Leu Met Ser Cys His His Asp Leu Val Phe Val Val Cys His
290 295 300

Leu Ile Ala Met Val Ser Thr Cys Ile Asn Pro Leu Phe Tyr Gly Phe
305 310 315 320

Leu Asn Lys Asn Phe Gln Lys Asp Leu Met Met Leu Ile His His Cys
325 330 335

Trp Cys Gly Glu Pro Gln Glu Ser Tyr Glu Asn Ile Ala Met Ser Thr
340 345 350

Met His Thr Asp Glu Ser Lys Gly Ser Leu Lys Leu Ala His Ile Pro
355 360 365

Thr Gly Ile
370